

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 01:38:52 ; Search time 124.25 Seconds
(without alignments)
49.507 Million cell updates/sec

Title: US-10-712-447-210
Perfect score: 20
Sequence: 1 XRRRXXXXXXXXX 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	95.0	133	7 ABO73099	Abo73099 Pseudomon
2	19	95.0	189	7 ABO83630	Abo83630 Pseudomon
3	19	95.0	323	8 ADX97192	Adx97192 Plant ful
4	19	95.0	442	7 ABO74539	Abo74539 Pseudomon
5	19	95.0	533	5 ADH48840	Adh48840 NOV53 pro
6	19	95.0	534	7 ADG48250	Adg48250 Human ret
7	19	95.0	644	4 AAU33234	Aau33234 Novel hum
8	19	95.0	19938	6 ABP76678	Abp76678 Streptom
9	18	90.0	15	5 AAB71432	Aab71432 Peptide A
10	18	90.0	16	5 AAB71430	Aab71430 Peptide T
11	18	90.0	19	3 AAY87840	Aay87840 Heparin b
12	18	90.0	19	5 AAB71428	Aab71428 Peptide B
13	18	90.0	59	5 ABP00279	Abp00279 Human ORF
14	18	90.0	64	8 ADX75905	Adx75905 Plant ful
15	18	90.0	77	4 AAU41918	Aau41918 Propionib
16	18	90.0	77	6 ABM38437	Abm38437 Propionib
17	18	90.0	78	5 ABP00666	Abp00666 Human ORF
18	18	90.0	89	4 AAU62059	Aau62059 Propionib
19	18	90.0	89	6 ABM58578	Abm58578 Propionib
20	18	90.0	93	5 ABP05425	Abp05425 Human ORF
21	18	90.0	103	7 ABO83790	Abo83790 Pseudomon
22	18	90.0	113	7 ABO68429	Abo68429 Pseudomon
23	18	90.0	127	4 AAU86821	Aau86821 Novel hum
24	18	90.0	127	7 ADB60155	Adb60155 Connectiv

25	18	90.0	134	7 ABO72505	Abo72505 Pseudomon
26	18	90.0	136	8 ADX87688	Adx87688 Plant ful
27	18	90.0	139	7 ABO78160	Abo78160 Pseudomon
28	18	90.0	139	7 ABO75935	Abo75935 Pseudomon
29	18	90.0	140	8 ADX78723	Adx78723 Plant ful
30	18	90.0	141	7 ABO74930	Abo74930 Pseudomon
31	18	90.0	142	7 ABO82700	Abo82700 Pseudomon
32	18	90.0	143	6 ABU11486	Abu11486 Human MDD
33	18	90.0	149	4 AAU42224	Aau42224 Propionib
34	18	90.0	149	6 ABM38743	Abm38743 Propionib
35	18	90.0	152	7 ABO76573	Abo76573 Pseudomon
36	18	90.0	152	8 ADX93670	Adx93670 Plant ful
37	18	90.0	207	7 ABO73028	Abo73028 Pseudomon
38	18	90.0	208	7 ABO68892	Abo68892 Pseudomon
39	18	90.0	209	7 ABO72617	Abo72617 Pseudomon
40	18	90.0	229	4 AAU47602	Aau47602 Propionib
41	18	90.0	229	6 ABM44121	Abm44121 Propionib
42	18	90.0	231	7 ABO68472	Abo68472 Pseudomon
43	18	90.0	237	7 ABO83595	Abo83595 Pseudomon
44	18	90.0	245	4 AAG90194	Aag90194 C glutami
45	18	90.0	255	8 ADY11827	Ady11827 Plant ful

ALIGNMENTS

RESULT 1
ABO73099
ID ABO73099 standard; protein; 133 AA.
XX
AC ABO73099;
XX
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #5274.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
PA Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
PI WPI; 2003-615309/58.
XX
DR N-PSDB; ABD06670.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 21845; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics, and
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide, of
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences

CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 133 AA;

Query Match 95.0%; Score 19; DB 7; Length 133;
 Best Local Similarity 33.3%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
 || ||
 Db 22 RRSARTSTRATR 33

RESULT 2
 ABO83630
 ID ABO83630 standard; protein; 189 AA.
 XX
 AC ABO83630;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polypeptide #15805.
 XX
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 XX
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 DR WPI; 2003-615309/58.
 XX
 DR N-ESDB; ABD17201.

Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 PT
 PS Disclosure; SEQ ID NO 32376; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 189 AA;

Query Match 95.0%; Score 19; DB 7; Length 189;

Best Local Similarity 33.3%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 Qy 3 RXXXXXXXXXR 14
 || ||
 Db 34 RRTSASARASR 45

RESULT 3
 ADX97192
 ID ADX97192 standard; protein; 323 AA.
 XX

AC ADX97192;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 59856.
 XX

KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX

OS Unidentified.
 XX
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 XX
 PR 05-NOV-2001; 2001US-00985678.

XX
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to
 XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 XX pests, for conferring increased resistance to plant disease, or for
 XX improving yield.

XX Claim 1; SEQ ID NO 59856; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
 XX polynucleotide consisting of a sequence encoding an amino acid sequence
 XX available in electronic form from the US patent office at
 XX ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 XX of the invention are also useful in physical arrays of molecules and as
 XX plant breeding markers. The recombinant DNA construct is useful for
 XX improving plant tolerance to cold, heat, drought, herbicides, extreme
 XX osmotic conditions, pathogens or pests, for manipulating growth rate in
 XX plant cells by modification of the cell cycle pathway, for conferring
 XX increased resistance to plant disease, for producing galactomannan,
 XX lignin or plant growth regulators, for increasing the rate of homologous
 XX recombination in plants, for improving yield by modification of
 XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 XX or by providing improved plant growth and development under at least one
 XX stress condition or for modifying seed oil or protein yield and/or
 XX content. This is the amino acid sequence of a plant full length insert
 XX polypeptide that can be used in the recombinant DNA construct of the

CC invention.
XX SQ Sequence 323 AA;
Query Match 95.0%; Score 19; DB 8; Length 323;
Best Local Similarity 33.3%; Pred. No. 3e+03; 8; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RXXXXXXXXX 14
DB 270 RRAASRSRTAR 281
RESULT 4
ID ABO74539 standard; protein; 442 AA.
XX ABO74539;
AC ABO74539;
DT 29-JUL-2004 (first entry)
DE Pseudomonas aeruginosa polypeptide #6714.
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
KW Pseudomonas aeruginosa.
OS US6551795-B1.
FN 22-APR-2003.
PD 18-FEB-1999; 99US-00252991.
PF 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
PI WPI; 2003-615309/58.
DR N-PSDB; ABD08110.
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX Disclosure; SEQ ID NO 23285; 455pp; English.
PS The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX Sequence 442 AA;
QY Query Match 95.0%; Score 19; DB 7; Length 442;
Best Local Similarity 33.3%; Pred. No. 3.9e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 RXXXXXXXXX 14

Db 307 RRAASRSRTAR 318
RESULT 5
ADH48840
ID ADH48840 standard; protein; 533 AA.
XX AC ADH48840;
XX 25-MAR-2004 (first entry)
XX NOV53 protein sequence, SEQ ID 124.
DE Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic;
KW hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV53;
KW protein-kinase-like protein; chromosome 20.
XX Homo sapiens.
OS WO200268652-A2.
FN 06-SEP-2002.
PD 26-FEB-2002; 2002WO-US005910.
PF 26-FEB-2001; 2001US-0271646P.
PR 27-FEB-2001; 2001US-0271840P.
PR 28-FEB-2001; 2001US-0272404P.
PR 28-FEB-2001; 2001US-0272405P.
PR 28-FEB-2001; 2001US-0272410P.
PR 28-FEB-2001; 2001US-0272414P.
PR 02-MAR-2001; 2001US-0272787P.
PR 02-MAR-2001; 2001US-0273048P.
PR 02-MAR-2001; 2001US-0273300P.
PR 16-MAR-2001; 2001US-0276401P.
PR 20-MAR-2001; 2001US-0278660P.
PR 30-MAR-2001; 2001US-0280039P.
PR 02-APR-2001; 2001US-0280818P.
PR 12-APR-2001; 2001US-0283443P.
PR 23-APR-2001; 2001US-0285754P.
PR 24-APR-2001; 2001US-0286096P.
PR 03-MAY-2001; 2001US-0288353P.
PR 17-MAY-2001; 2001US-0291703P.
PR 31-MAY-2001; 2001US-0294834P.
PR 20-JUN-2001; 2001US-0299695P.
PR 21-JUN-2001; 2001US-0299845P.
PR 05-JUL-2001; 2001US-0303242P.
PR 13-AUG-2001; 2001US-0311981P.
PR 16-AUG-2001; 2001US-0312858P.
PR 17-AUG-2001; 2001US-0313280P.
PR 29-AUG-2001; 2001US-0315614P.
PR 17-SEP-2001; 2001US-0322818P.
PR 25-FEB-2002; 2002US-00322818.
XX (CURA-) CURAGEN CORP.
PA Alsobrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE;
PI Casman SJ, Ellerman KE, Gangolli EA, Gerlach VL, Gilbert JA;
PI Gorman L, Guo X, Gusev VV, Kekuda R, Li L, Liu X, Malyankar UM;
PI Miller CE, Millet I, Padigaru M, Patturajan M, Pena CE, Peyman JA;
PI Rascelli L, Shenoy SG, Shinkets RA, Smithson G, Spytek KA, Stone DJ;
PI Taupier RJ, Tchernev VT, Vernet CAM, Zernhusen BD;
XX WPI; 2002-698672/75.
DR N-PSDB; ADH48839.
XX New NOVX polypeptides or polynucleotides, useful for preventing or
PT treating disorders or syndromes e.g., atherosclerosis, hypertension,
PT obesity or cancer.

```

XX PS Claim 1; Page 298; 923pp; English.
XX CC The present invention relates to novel human NOVX proteins, where X is
XX CC any number from 1 to 91 and their coding sequences. The proteins and
XX CC coding sequences are useful for preventing or treating disorders or
XX CC syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV53 is
XX CC a protein kinase-like protein and its coding sequence maps to chromosome
XX CC 20.
XX SQ Sequence 533 AA;
    Query Match          95.0%; Score 19; DB 5; Length 533;
    Best Local Similarity 33.3%; Pred. No. 4.5e+03;
    Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RXXXXXXXXXXR 14
Db 56 RRARAATSRAR 67

RESULT 6
ADG48250
ID ADG48250 standard; protein; 534 AA.
XX AC ADG48250;
XX DT 11-MAR-2004 (first entry)
XX DE Human retina-specific protein kinase A203.
XX KW human; retina-specific protein; NET01; retinal disease;
XX KW age related macular degeneration; night blindness; protein kinase A203.
XX OS Homo sapiens.
XX PN WO2003068967-A2.
XX PD 21-AUG-2003.
XX PF 18-FEB-2003; 2003WO-EP001625.
XX PR 18-FEB-2002; 2002EP-00003675.
XX PR 21-FEB-2002; 2002US-0357857P.
XX PA (LYNK-) LYNKEUS BIO TECH GMBH.
XX PI Stoehr BH, Weber FHB, Goehring F;
XX DR N-PSDB; ADG48249.
XX DR WPI; 2003-767334/72.
XX PT New nucleic acid encoding retinal protein sNET01, useful for diagnosis of
XX PT retinal disease, especially macular degeneration, also for drug screening
XX PT and therapy.
XX PS Claim 18; Fig 6; 199pp; English.
XX CC The invention comprises the amino acid and coding sequences of a human
XX CC retina-specific protein - NET01. The DNA and protein sequences of the
XX CC invention are useful in the treatment of retinal diseases, such as
XX CC macular degeneration (especially age related) and night blindness. The
XX CC present amino acid sequence represents human retina-specific protein
XX CC kinase A203.
XX SQ Sequence 534 AA;
    Query Match          95.0%; Score 19; DB 7; Length 534;
    Best Local Similarity 33.3%; Pred. No. 4.5e+03;
    Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RXXXXXXXXXXR 14
Db 56 RRARAATSRAR 67

RESULT 7
AAU33234
ID AAU33234 standard; protein; 644 AA.
XX AC AAU33234;
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #3725.
XX KW Human; vaccination; gene therapy; nutritional supplement;
XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS Homo sapiens.
XX PN WO200179449-A2.
XX PD 25-OCT-2001.
XX PF 16-APR-2001; 2001WO-US008656.
XX PR 18-APR-2000; 2000US-00552929.
XX PR 26-JAN-2001; 2001US-00770160.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-611725/70.
XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX PT vaccination, testing and therapy.
XX PS Claim 20; Page 738-739; 765pp; English.
XX CC The invention relates to novel human secreted polypeptides. The
XX CC polypeptides and antibodies to the polypeptides are useful for
XX CC determining the presence of or predisposition to a disease associated
XX CC with altered levels of polypeptide. The polypeptides are also useful for
XX CC identifying agents (agonists and antagonists) that bind to them. Cells
XX CC expressing the proteins are useful for identifying a therapeutic agent
XX CC for use in treatment of a pathology related to aberrant expression or
XX CC physiological interactions of the polypeptide. Vectors comprising the
XX CC nucleic acids encoding the polypeptides and cells genetically engineered
XX CC to express them are also useful for producing the proteins. The proteins
XX CC are useful in genetic vaccination, testing and therapy, and can be used
XX CC as nutritional supplements. They may be used to increase stem cell
XX CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX CC and/or nerve tissue growth or regeneration; immune suppression and/or
XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX CC AAU29510-AAU33304 represent the amino acid sequences of novel human
XX CC secreted proteins of the invention
XX SQ Sequence 644 AA;
    Query Match          95.0%; Score 19; DB 4; Length 644;
    Best Local Similarity 33.3%; Pred. No. 5.2e+03;
    Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RXXXXXXXXXXR 14
Db 46 RRRRAAARAAAR 57

RESULT 8
ABP76678
ID ABP76678 standard; protein; 19938 AA.
XX AC ABP76678;

```

XX 26-FEB-2003 (first entry)
DT Streptomyces viridochromogenes Avi gene cluster polypeptide frame 2.
DE
XX Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection;
KW medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.
KW
XX Streptomyces viridochromogenes.
OS
XX WO2000268436-A1.
PN
XX 06-SEP-2002.
PD
XX 24-AUG-2001; 2001WO-EP009815.
PF
XX 25-FEB-2001; 2001DE-01009166.
PR
XX (COMB-) COMBINATURE BIOPHARM AG.
PA
XX Weitnauer G, Muehlenweg A, Trefzer A, Bechthold A;
PI
XX WPI; 2003-018650/01.
XX N-PSDB; ABZ37515.
DR
XX New avilamycin derivatives, useful for treatment of infections, and
PT nucleic acid encoding avilamycin synthesis enzymes.
PT
XX Example 1; Page 68-301; 319pp; German.
PS
XX The invention relates to avilamycin derivatives (I) with antibacterial,
CC virucide, protozoacide and fungicide activity. (I) are useful for
CC treatment of infections (bacterial, viral, protozoal or fungal), in human
CC or veterinary medicine, particularly where caused by Staphylococcus
CC aureus. (I) are more hydrophilic than known avilamycins. The present
CC sequence is that of an avilamycin synthesis enzyme from the Streptomyces
CC viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-
XX ABZ37516)
XX
SQ Sequence 19938 AA;
Query Match 95.0%; Score 19; DB 6; Length 19938;
Best Local Similarity 33.3%; Pred. No. 7.6e+04;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 RXXXXXXXXX 14
DB 11248 RRRSSTASRTSR 11259
RESULT 9
AAB71432
ID AAB71432 standard; peptide; 15 AA.
AC AAB71432;
XX
XX 27-NOV-2002 (first entry)
DT
DE Peptide Arg Helix #3 for construction of Tris-Arg helix #3.
XX
KW Sepsis; branched chain peptide; antibacterial; immunosuppressive;
KW endotoxin; helix peptide.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "This residue has a side chain C(O)-NepsilonH-
FT (CH2)3-Tris-ArgHel#3, where the Tris-ArgHel#3 is
FT represented in AAB71431"
FT Modified-site 16
FT /note= "Acylated residue"
XX

PN EP1232754-A2.
XX
PD 21-AUG-2002.
XX
XX 14-FEB-2002; 2002EP-00251027.
PF
XX 14-FEB-2001; 2001US-0268410P.
XX
XX (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
PA
XX Harris RB, Wolz RL, Wolz G;
XX WPI; 2002-659478/71.
PI
DR
XX Use of cationic helix peptides for treatment of sepsis and for the
PT detection and removal of endotoxins.
PT
XX Disclosure; Fig 2; 18pp; English.
PS
XX This invention describes a novel use of antibacterial and
CC immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra
CC -Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for
CC the treatment of sepsis and the detection and removal of endotoxins. The
CC peptides of the invention are used in a method for detecting endotoxin in
CC a sample comprising contacting the sample with a labelled helix peptide
CC and then detecting the presence of any labelled molecule bound to
CC endotoxin. The peptides can also be used in a method for removing
CC endotoxin in a sample which comprises exposing the sample to a helix
CC peptide, bound to a solid support, then collecting the sample. The
CC endotoxin removal may be in vivo, or the peptides may be used to form an
CC affinity trap for endotoxins in e.g. dialysis-type treatments, or for
CC removal of endotoxins from plasma fractionation products. They are also
CC used as model frameworks for endotoxin binding from which new analogues
CC may be designed. This sequence represents the peptide Arg Helix #3 which
CC is used in the construction of the branched chain peptide Tris-Arg Helix
CC #3 described in the method of the invention
XX
SQ Sequence 15 AA;
Query Match 90.0%; Score 18; DB 5; Length 15;
Best Local Similarity 33.3%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 RXXXXXXXXX 14
DB 1 RRAAARAAARRAR 12
RESULT 10
AAB71430
ID AAB71430 standard; peptide; 16 AA.
XX
XX AAB71430;
AC
XX 27-NOV-2002 (first entry)
DT
XX Peptide Tris-Arg Helix #3 fragment.
DE
XX Sepsis; branched chain peptide; antibacterial; immunosuppressive;
KW endotoxin; helix peptide.
KW
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 16
FT /note= "Ala is modified by unidentified R1 group"
XX
XX EP1232754-A2.
PN
XX 21-AUG-2002.
PD
XX 14-FEB-2002; 2002EP-00251027.
XX

PR 14-FEB-2001; 2001US-0268410P.
XX (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
XX Harris RB, Wolz RL, Wolz G;
XX WPI; 2002-659478/71.
XX Use of cationic helix peptides for treatment of sepsis and for the
PT detection and removal of endotoxins.
XX
XX Disclosure; Fig 1B; 18pp; English.
XX
XX This invention describes a novel use of antibacterial and
CC immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra
CC -Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for
CC the treatment of sepsis and the detection and removal of endotoxins. The
CC peptides of the invention are used in a method for detecting endotoxin in
CC a sample comprising contacting the sample with a labelled helix peptide
CC and then detecting the presence of any labelled molecule bound to
CC endotoxin. The peptides can also be used in a method for removing
CC endotoxin in a sample which comprises exposing the sample to a helix
CC peptide, bound to a solid support, then collecting the sample. The
CC endotoxin removal may be in vivo, or the peptides may be used to form an
CC affinity trap for endotoxins in e.g. dialysis-type treatments, or for
CC removal of endotoxins from plasma fractionation products. They are also
CC used as model frameworks for endotoxin binding from which new analogues
CC may be designed. This sequence represents the peptide Arg Helix #3 which
CC is used in the construction of Tris-Arg Helix #3, a branched chain
CC peptide described in the method of the invention
XX
XX Sequence 16 AA;
SQ

Query Match 90.0%; Score 18; DB 5; Length 16;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RXXXXXXXRXR 14
Db 2 RRAAARAAARRAR 13

RESULT 11
AA87840
ID AA87840 standard; peptide; 19 AA.
AC AA87840;
XX
XX 01-SEP-2000 (first entry)
XX Heparin binding peptide Bis-Arg helix #2.
XX
XX Heparin binding peptide; antagonist; cardiovascular; coagulant;
KW bleeding wound; vascular anastomoses; leaking prosthetic vascular graft;
KW protamine substitute; treatment.
XX
XX Synthetic.
OS
XX
XX EP999219-A2.
XX
XX 10-MAY-2000.
XX
XX 01-OCT-1999; 99EP-00119514.
XX
XX 06-OCT-1998; 98US-00166930.
XX
XX (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
XX
XX Harris RB, Sobel M;
XX WPI; 2000-306006/27.
XX
XX New heparin binding molecules, useful for reducing heparin content in a

PT mammal by reducing the anticoagulant effects of heparin.
XX
XX Example 1; Fig 1a; 39pp; English.
XX
XX This invention describes novel heparin binding molecules (I). The
CC molecules (I) are useful as heparin antagonist drugs for cardiovascular
CC application and specifically neutralize heparin's conventional
CC anticoagulant properties. (I) are also useful for counteracting actions
CC of heparin locally e.g. in bleeding wounds, vascular anastomoses or
CC leaking prosthetic vascular grafts. (I) is also useful combined in a
CC pharmaceutical composition with insulin, as a substitute for protamine
CC for use in treating diabetics. The heparin binding molecules (I)
CC specifically neutralize heparin's conventional anticoagulant properties
CC without causing deleterious hemodynamic side-effects or exacerbation of
CC the proliferative vascular response to injury. (I) are short-duration,
CC intravenous drugs to be used in elective or emergency situations which
CC can safely and specifically neutralize heparin's proliferative response
CC to injury. This sequence represents a heparin-binding peptide described
CC in the method of the invention
XX
XX Sequence 19 AA;
SQ

Query Match 90.0%; Score 18; DB 3; Length 19;
Best Local Similarity 33.3%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RXXXXXXXRXR 14
Db 5 RRAAARAAARRAR 16

RESULT 12
AA871428
ID AA871428 standard; peptide; 19 AA.
XX
XX AA871428;
XX
XX 27-NOV-2002 (first entry)
XX
XX Peptide Bis-Arg Helix #2 fragment #1.
XX
XX Sepsis; branched chain peptide; antibacterial; immunosuppressive;
KW endotoxin; helix peptide.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 19
FT /note= "Ala is modified by unidentified R1 group"
XX
XX EP1232754-A2.
XX
XX 21-AUG-2002.
XX
XX 14-FEB-2002; 2002EP-00251027.
XX
XX 14-FEB-2001; 2001US-0268410P.
XX
XX (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
XX
XX Harris RB, Wolz RL, Wolz G;
XX
XX WPI; 2002-659478/71.
XX
XX Use of cationic helix peptides for treatment of sepsis and for the
PT detection and removal of endotoxins.
XX
XX Disclosure; Fig 1A; 18pp; English.
XX
XX This invention describes a novel use of antibacterial and
CC immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra
CC -Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for
CC the treatment of sepsis and the detection and removal of endotoxins. The

peptides of the invention are used in a method for detecting endotoxin in a sample comprising contacting the sample with a labelled helix peptide and then detecting the presence of any labelled molecule bound to endotoxin. The peptides can also be used in a method for removing endotoxin in a sample which comprises exposing the sample to a helix peptide, bound to a solid support, then collecting the sample. The endotoxin removal may be in vivo, or the peptides may be used to form an affinity trap for endotoxins in e.g. dialysis-type treatments, or for removal of endotoxins from plasma fractionation products. They are also used as model frameworks for endotoxin binding from which new analogues may be designed. This sequence represents the peptide Arg Helix #2 which is used in the construction of B1s-Arg Helix #2, a branched chain peptide described in the method of the invention

Sequence 19 AA;

Query Match 90.0%; Score 18; DB 5; Length 19;
Best Local Similarity 33.3%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 5 RRAAARARRR 16

RESULT 13

ABP00279
ID ABP00279 standard; protein; 59 AA.

AC ABP00279;

DT 24-JUN-2002 (first entry)

DE Human ORFX protein sequence SEQ ID NO:540.

Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.

OS Homo sapiens.

XX WO200192523-A2.

PN 06-DEC-2001.

PD 29-MAY-2001; 2001WO-US010836.

PF 30-MAY-2000; 2000US-0206132P.

PR 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach MD;

XX WPI; 2002-106308/14.

DR N-PSDB; ABN16031.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.

PS Disclosure; SEQ ID NO 540; 1037pp; English.

XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated

disorder in humans, and in the manufacture of a medicament for treating a
syndrome associated with ORFX-associated disorder. ORFX polynucleotide
sequences can be used in gene therapy. ORFX sequences can be used in the
treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
osteoarthritis, neurodegenerative disorders, disorders related to organ
transplantation, cardiovascular diseases, diabetes mellitus, systemic
lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
storage disease, various immune deficiencies and disorders, rheumatoid
diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
disease and autoimmune inflammatory eye disease. ORFX proteins are also
useful for treating burns, incisions, ulcers, for treating osteoporosis,
bone degenerative disorders, or periodontal disease, and for gut
protection or regeneration and treatment of lung or liver fibrosis,
reperfusion injury in various tissues and conditions resulting from
systemic cytokine damage. N.B. The sequence data for this patent did not
form part of the printed specification, but was obtained in electronic
format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 59 AA;

Query Match 90.0%; Score 18; DB 5; Length 59;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 43 RRSRTARASR 54

RESULT 14

ADX75905
ID ADX75905 standard; protein; 64 AA.

AC ADX75905;

DT 21-APR-2005 (first entry)

DE Plant full length insert polypeptide seqid 45271.

plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.

OS Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.

PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.

PA (TAB/) TABASKA J E.

PA (CAOY/) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

XX
 PS Claim 1; SEQ ID NO 45271; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX SQ Sequence 64 AA;

Query Match 90.0%; Score 18; DB 8; Length 64;
 Best Local Similarity 33.3%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
 |||||
 Db 19 RRTSSRRTRATR 30

RESULT 15

AAU41918
 ID AAU41918 standard; protein; 77 AA.

XX
 AC AAU41918;

DT 13-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #2814.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US012865.

XX 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

DR N-PSDB; AAS59515.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris.

XX Example 1; SEQ ID NO 3113; 1069pp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 77 AA;

Query Match 90.0%; Score 18; DB 4; Length 77;
 Best Local Similarity 33.3%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
 |||||
 Db 39 RRSMASTARSGR 50

Search completed: March 29, 2006, 01:44:11
 Job time : 127.25 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 01:44:43 ; Search time 20.5625 Seconds
(without alignments)
65.509 Million cell updates/sec

Title: US-10-712-447-210

Perfect score: 20

Sequence: 1 XRRXXXXXXXXX 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	90.0	79	2 S65036	nuclear basic prot
2	18	90.0	79	2 JH0404	basic nuclear prot
3	18	90.0	110	2 T30752	hypothetical prote
4	18	90.0	197	2 T18918	hypothetical prote
5	18	90.0	474	1 BVRCE	cyab protein - Bor
6	18	90.0	574	2 T14162	hABC transport pro
7	18	90.0	660	2 D72453	hypothetical prote
8	18	90.0	668	2 A13144	two component sens
9	18	90.0	710	2 B98143	cvgsy protein (AE0
10	17	85.0	195	2 G72697	hypothetical prote
11	17	85.0	207	2 D87267	hypothetical prote
12	17	85.0	238	2 A57198	splicing factor, a
13	17	85.0	241	2 G70705	hypothetical prote
14	17	85.0	310	2 T29423	probable transposa
15	17	85.0	317	2 PQ0339	hypothetical prote
16	17	85.0	344	2 S59043	spilling factor SR
17	17	85.0	395	2 E82796	hypothetical prote
18	17	85.0	436	2 T36706	hypothetical prote
19	17	85.0	461	2 A70837	probable proteinase
20	17	85.0	520	2 E87435	conserved hypothet
21	17	85.0	571	2 T40911	probable PHD-type
22	17	85.0	717	2 T15340	hypothetical prote
23	17	85.0	724	2 B85045	probable calcium c
24	17	85.0	1017	2 T13354	probable potassium
25	17	85.0	1577	2 T13722	hypothetical prote
26	17	85.0	1622	2 JE0378	DNA (cytosine-5)-
27	17	85.0	2351	2 G71415	hypothetical prote
28	17	85.0	3144	2 A46068	Huntington disease
29	16	80.0	52	2 FN0081	sperm chromatin pr

ALIGNMENTS

RESULT 1

S65036

nuclear basic protein SP4, sperm-specific - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C:Accession: S65036

R:Mita, K.; Ariyoshi, N.; Abe, S.; Takamune, K.; Katagiri, C.

Biochim. Biophys. Acta 1245, 430-438, 1995

A>Title: Structure of genes for sperm-specific nuclear basic protein (SP4) in Xenopus la

A:Reference number: S65036; MUID:96125743; PMID:8541323

A:Accession: S65036

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-79 <MIT>

A:Cross-references: UNIPARC:UPI000017BF96; EMBL:D45253

A>Note: the authors translated the codon TAT for residue 73 as Thr

C:Genetics:

A:Gene: XLSP41

A:Introns: 76/1

Query Match 90.0%; Score 18; DB 2; Length 79;

Best Local Similarity 33.3%; Pred. No. 46;

Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14

DB 45 RRARTSTARRAR 56

RESULT 2

JH0404

basic nuclear protein SP4 precursor, sperm-specific - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: JH0404; PU0021; S65037; S65038; S65039

R:Hiyoshi, H.; Uno, S.; Yokota, T.; Katagiri, C.; Nishida, H.; Takai, M.; Agata, K.; Egu

Exp. Cell Res. 194, 95-99, 1991

A>Title: Isolation of cDNA for a Xenopus sperm-specific basic nuclear protein (SP4) and

A:Reference number: JH0404; MUID:91200205; PMID:2015853

A:Accession: JH0404

A:Molecule type: mRNA

A:Residues: 1-79 <HY>

A:Cross-references: UNIPROT:P24056; UNIPARC:UPI000000D6D6; GB:D00916; NID:G222970; PIDN

A:Experimental source: round spermatid

A:Accession: PU0021

A:Molecule type: protein

A:Residues: 2-11;12-43;65-74;75-79 <H12>

A:Cross-references: UNIPARC:UPI000017BF78; UNIPARC:UPI000017BF79; UNIPARC:UPI000017BF7A;

R:Mita, K.; Ariyoshi, N.; Abe, S.; Takamune, K.; Katagiri, C.

Biochim. Biophys. Acta 1245, 430-438, 1995

A>Title: Structure of genes for sperm-specific nuclear basic protein (SP4) in Xenopus la

A:Reference number: S65036; MUID:96125743; PMID:8541323

A:Accession: S65036

A;Accession: S65037	
A;Molecule type: DNA	
A;Residues: 1-79 <MIT>	
A;Cross-references: UNIPARC:UPI00000D6D6; EMBL:D45253; NID:g639883; PIDN:BAA08209.1; PT	
A;Experimental source: strain J	
A;Genetics: CH1	
A;Note: the authors translated the codon TAT for residue 73 as Thr	
A;Accession: S65038	
A;Molecule type: DNA	
A;Residues: 1-79 <MIS>	
A;Cross-references: UNIPARC:UPI00000D6D6; EMBL:D45253; NID:g639883; PIDN:BAA08209.1; PT	
A;Experimental source: strain J	
A;Genetics: CH2	
A;Note: the authors translated the codon TAT for residue 73 as Thr	
A;Accession: S65039	
A;Molecule type: DNA	
A;Residues: 1-79 <MIW>	
A;Cross-references: UNIPARC:UPI00000D6D6; EMBL:D45253; NID:g639883; PIDN:BAA08209.1; PT	
A;Experimental source: strain J	
A;Genetics: CH3	
A;Note: the authors translated the codon TAT for residue 73 as Thr	
C;Genetics: <CH1>	
A;Gene: XLSP42	
A;Introns: 76/1	
C;Genetics: <CH2>	
A;Gene: XLSP43	
A;Introns: 76/1	
C;Genetics: <CH3>	
A;Gene: XLSP44	
A;Introns: 76/1	
C;Keywords: sperm	
F;2-79/Product: basic nuclear protein SP4 #status experimental <MAT>	
Query Match	90.0%; Score 18; DB 2; Length 79;
Best Local Similarity	33.3%; Pred.No. 46;
Matches	4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy	3 RXXXXXXXXXXR 14
Dd	45 RRARTSTARRAR 56
RESULT 3	
T30752	
hypothetical protein 150R - Molluscum contagiosum virus 1	
N;Alternate names: MC150R	
C;Species: Molluscum contagiosum virus 1	
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004	
C;Accession: T30752	
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.	
Science 273, 813-816, 1996	
A>Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re	
A;Reference number: Z20876; MUID:96325459; PMID:8670425	
A;Accession: T30752	
A>Status: preliminary; translated from GE/EMBL/DDBJ	
A:Molecule type: DNA	
A;Residues: 1-110 <SEN>	
A;Cross-references: UNIPROT:Q98316; UNIPARC:UPI00000EBCB2C; EMBL:U60315; NID:gl491943; PT	
C;Genetics:	
A;Note: MC150R	
C;Superfamily: Molluscum contagiosum virus 1 hypothetical protein 150R	
Query Match	90.0%; Score 18; DB 2; Length 110;
Best Local Similarity	33.3%; Pred.No. 61;
Matches	4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy	3 RXXXXXXXXXXR 14
Dd	86 RRAHAARAARRAR 97
RESULT 4	
T18918	

```
Query Match      90.0%; Score 18; DB 2; Length 574;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXXR 14
Db 233 RRLTATLRAAR 244

RESULT 7
D72453
hypothetical protein APE2272 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C:Accession: D72453
R;Kawarayayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: D72453
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-660 <KAW>
A:Cross-references: UNIPROT:Q9Y9L6; UNIPARC:UPI000005E2A0; DDBJ:AP0000064; NID:G5105945;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2272
F;459-644/Domain: ATP-binding cassette homology <ABC>

Query Match      90.0%; Score 18; DB 2; Length 660;
Best Local Similarity 33.3%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXXR 14
Db 293 RRNTAAARIAR 304

RESULT 8
AI3144
two component sensor kinase Atu4781 [imported] - Agrobacterium tumefaciens (strain C58,
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AI3144
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AI3144
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-668 <KUR>
A:Cross-references: UNIPROT:Q8UGM6; UNIPARC:UPI00001649AC; GB:AE008689; PIDN:AAL45575.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4781
A:Map position: linear chromosome

Query Match      90.0%; Score 18; DB 2; Length 668;
Best Local Similarity 33.3%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXXR 14
Db 313 RRTAEAAARTIR 324
```

```
RESULT 9
B98143
cvdS protein (AE006176) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B98143
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B98143
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-710 <KUR>
A:Cross-references: UNIPROT:Q8UGM6; UNIPARC:UPI000000D26D3; GB:AE007870; PIDN:AAK88668.1;
C:Genetics:
A:Gene: AGR_L_203
A:Map position: linear chromosome

Query Match      90.0%; Score 18; DB 2; Length 710;
Best Local Similarity 33.3%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXXR 14
Db 355 RRTAEAAARTIR 366

RESULT 10
G72697
hypothetical protein APE0999 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: G72697
R;Kawarayayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72697
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <KAW>
A:Cross-references: UNIPROT:Q9YDB4; UNIPARC:UPI000005DD8C; DDBJ:AP0000060; NID:G5104188;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0999

Query Match      85.0%; Score 17; DB 2; Length 195;
Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXXR 14
Db 12 RRSMLTSRRSSR 23

RESULT 11
D87267
hypothetical protein CC0149 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: D87267
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; MUID:21173698; PMID:11259647
A:Accession: D87267
A>Status: preliminary
A:Molecule type: DNA
```

A;Residues: 1-207 <STO>
A;Cross-references: UNIPROT:Q9ABSI; UNIPARC:UPI00000C6F4B; GB:AE005673; NID:g13421262; P
C;Genetics:
A;Gene: CC0149

Query Match 85.0%; Score 17; DB 2; Length 207;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXXR 14
|||
Db 2 RRSRSTRSRETR 13

RESULT 12
A57198
splicing factor, arginine/serine-rich 7 - human
N;Alternate names: splicing factor 9G8
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 31-Dec-2004
C;Accession: A57198; S46319
R;Popielarz, M.; Cavaloc, Y.; Mattei, M.G.; Gattoni, R.; Stevenin, J.
J. Biol. Chem. 270, 17830-17835, 1995
A;Title: The gene encoding human splicing factor 9G8. Structure, chromosomal localization
A;Reference number: A57198; MUID:95355374; PMID:7629084
A;Accession: A57198
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-238 <RES>
A;Cross-references: UNIPROT:Q16629; UNIPARC:UPI00000D853; GB:L41887; NID:g950423; PIDN:
R;Cavaloc, Y.; Popielarz, M.; Fuchs, J.P.; Gattoni, R.; Stevenin, J.
EMBO J. 13, 2639-2649, 1994
A;Title: Characterization and cloning of the human splicing factor 9G8: a novel 35 kDa f
A;Reference number: S46319; MUID:94283389; PMID:8013463
A;Accession: S46319
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-238 <CAV>
A;Cross-references: UNIPARC:UPI00000D853; EMBL:L22253; NID:g506401; PIDN:AAA35495.1; PI
C;Genetics:
A;Gene: GDB:SFRS7; 9G8
A;Cross-references: GDB:378350; OMIM:600572
A;Map position: 2p22-2p21
A;Introns: 10/1; 70/2; 129/2; 154/2; 191/2; 209/2; 221/2
F;12-74/Domain: ribonucleoprotein repeat homology <RRM3>

Query Match 85.0%; Score 17; DB 2; Length 238;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXXR 14
|||
Db 169 RRSRSASLRSR 180

RESULT 13
G70705
hypothetical protein Rv0756c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: G70705
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70705
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-241 <COL>
A;Cross-references: UNIPROT:P71813; UNIPARC:UPI00000D46FB; GB:Z80226; GB:AL123456; NID:g

A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv0756c

Query Match 85.0%; Score 17; DB 2; Length 241;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXXR 14
|||
Db 225 RRSRSRVSQR 236

RESULT 14
T29423
probable transposase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29423
R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A;Reference number: Z20619
A;Accession: T29423
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-310 <PAR>
A;Cross-references: UNIPROT:O86606; UNIPARC:UPI00000DAD10; EMBL:AL031155; NID:el313489; I
C;Genetics:
A;Note: SC3A7.05c

Query Match 85.0%; Score 17; DB 2; Length 310;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXXR 14
|||
Db 262 RRRTPASARSAR 273

RESULT 15
PQ0339
hypothetical protein 317 - Lymantria dispar nuclear polyhedrosis virus (fragment)
N;Alternate names: ORFA protein
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: PQ0339
R;Bjornson, R.M.; Rohrmann, G.F.
J. Gen. Virol. 73, 1499-1504, 1992
A;Title: Nucleotide sequence of the polyhedron envelope protein gene region of the Lymantria
A;Reference number: PQ0339; MUID:92300345; PMID:1607868
A;Accession: PQ0339
A;Molecule type: DNA
A;Residues: 1-317 <BJO>
A;Cross-references: UNIPARC:UPI00017A7C2; DBJ:D10836

Query Match 85.0%; Score 17; DB 2; Length 317;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXXR 14
|||
Db 9 RRADGASARRSR 20

Search completed: March 29, 2006, 01:50:04
Job time : 21.5625 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 01:39:37 ; Search time 129.062 Seconds
(without alignments)
76.532 Million cell updates/sec

Title: US-10-712-447-210

Perfect score: 20

Sequence: 1 XRRRXXXXXXRXR 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	414	Q4NWE6_9DEL	Q4NWE6 anaeromyxob
2	20	100.0	452	Q7RWX1_NEUCR	Q7RWX1 neurospora
3	20	100.0	994	Q95SV1_CAEEL	Q95SV1 caenorhabdi
4	20	100.0	1139	Q4SDD4_TETNG	Q4SDD4 tetradon n
5	19	95.0	194	Q74EX0_GEOSL	Q74EX0 geobacter s
6	19	95.0	214	Q7FOM2_ORYSA	Q7FOM2 oryza sativ
7	19	95.0	444	Q4LNR3_9BURK	Q4LNR3 burkholderi
8	19	95.0	497	AMPA_SYNEL	Q86I46 synechococc
9	19	95.0	817	PERQ1_HUMAN	Q75420 homo sapien
10	19	95.0	833	Q4QE71_LEIMA	Q4QE71 leishmania
11	19	95.0	856	Q4NSL6_9DEL	Q4NSL6 anaeromyxob
12	18	90.0	57	Q5N831_ORYSA	Q5N831 oryza sativ
13	18	90.0	78	SP4_XENLA	P24056 xenopus lae
14	18	90.0	79	Q53X49_XENLA	Q53X49 xenopus lae
15	18	90.0	85	Q6XN62_RHOER	Q6XN62 rhodococcus
16	18	90.0	102	Q62BE3_BURMA	Q62BE3 burkholderi
17	18	90.0	109	Q211376_MCV1	O11376 molluscum c
18	18	90.0	110	Q98316_MCV1	Q98316 molluscum c
19	18	90.0	112	Q52840_ORYSA	Q52840 oryza sativ
20	18	90.0	115	Q6TWS5_9POXV	Q6TWS5 orf virus
21	18	90.0	120	Q4NDP5_9MICC	Q4NDP5 arthrobacte
22	18	90.0	133	Q69MP7_ORYSA	Q69MP7 oryza sativ
23	18	90.0	138	Q7X8A7_ORYSA	Q7X8A7 oryza sativ
24	18	90.0	146	Q4N8B7_THEPA	Q4N8B7 theileria p
25	18	90.0	183	VC07_ADEB2	Q96624 bovine aden
26	18	90.0	183	Q7M6E8_ADEB2	Q7M6E8 bovine aden
27	18	90.0	188	Q5ZD02_ORYSA	Q5ZD02 oryza sativ
28	18	90.0	190	Q8LMA3_ORYSA	Q8LMA3 oryza sativ
29	18	90.0	190	Q62AV1_BURMA	Q62AV1 burkholderi
30	18	90.0	193	Q7G4Q0_ORYSA	Q7G4Q0 oryza sativ
31	18	90.0	197	Q17626_CAEEL	Q17626 caenorhabdi

Q7EVP7 oryza sativ
Q8LHV7 oryza sativ
Q63X19 burkholderi
Q5Y8D5 nocardia fa
Q828F2 streptomyce
Q5B410 aspergillus
Q9RJ76 streptomyce
Q6EQ52 oryza sativ
Q5W6D5 oryza sativ
Q4NTS2 anaeromyxob
Q4LPK5 burkholderi
Q4IQ72 gibberella
P11092 bordetella
Q7W1M9 bordetella

32 18 90.0 197 2 Q7EVP7 ORYSA
33 18 90.0 210 2 Q8LHV7 ORYSA
34 18 90.0 210 2 Q63X19 BURPS
35 18 90.0 216 2 Q5Y8D5 NOCPA
36 18 90.0 226 2 Q828F2 STRAM
37 18 90.0 313 2 Q5B410 EMENI
38 18 90.0 344 2 Q9RJ76 STRCO
39 18 90.0 348 2 Q6EQ52 ORYSA
40 18 90.0 352 2 Q5W6D5 ORYSA
41 18 90.0 392 2 Q4NTS2 9DEL
42 18 90.0 447 2 Q4LPK5 9BURK
43 18 90.0 462 2 Q4IQ72 GIBZE
44 18 90.0 474 1 CYAE BORPE
45 18 90.0 474 2 Q7W1M9 BORPA

ALIGNMENTS

RESULT 1
Q4NWE6_9DEL PRELIMINARY; PRT; 414 AA.
AC Q4NWE6;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE ATP-binding region, ATPase-like:Histidine Kinase A, N-terminal precursor.
DE ORFNames=AdehDRAFT_3131;
GN Anaeromyxobacter dehalogenans 2CP-C.
OS Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C";
RT dehalogenans 2CP-C";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C";
RT dehalogenans 2CP-C";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDA whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; AAHD01000008; EAL79882.1; -; Genomic_DNA.
DR ATP-binding; Kinase; Signal.
KW SIGNAL
FT SIGNAL 1 32
SQ SEQUENCE 414 AA; 41594 MW; 0ADF0F0DCA0B0C53 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 414;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RRRXXXXXXRXR 14
DB 189 RRRSAAAAAAR 200

RESULT 2
Q7RWX1_NEUCR PRELIMINARY; PRT; 452 AA.
ID Q7RWX1;
AC Q7RWX1;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU08793.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kanvassellis M., Mauceli E., Bielek C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Sella A., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbel D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000758; EAA27000.1; -; Genomic DNA.
SQ SEQUENCE 452 AA; 47319 MW; F1737BBSA311FC3 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 452;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXRXR 14
DB 347 RRSSTTTTTRAR 358

RESULT 3
ID Q96SV1_CABEL PRELIMINARY; PRT; 994 AA.
AC Q96SV1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein Y48G1B.5.
GN ORFNames=Y48G1B.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AC024794; AAK68497.1; -; Genomic DNA.
DR Ensembl; Y48G1B.5; Caenorhabditis elegans.
DR WormBase; WBGene00021670; Y48G1B.5.
DR WormPep; Y48G1B.5; CE26117.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 994 AA; 111289 MW; 73F6FC32D71D5CCC CRC64;

Query Match 100.0%; Score 20; DB 2; Length 994;
Best Local Similarity 33.3%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXRXR 14
DB 161 RRSSTTTTTRAR 172

RESULT 5
ID Q74EX0_GEOSL PRELIMINARY; PRT; 194 AA.
AC Q74EX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=GSU0839;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.

Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 RXXXXXXRXR 14
DB 161 RRSSTTTTTRAR 172

Query Match 100.0%; Score 20; DB 2; Length 1139;
Best Local Similarity 33.3%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXRXR 14
DB 161 RRSSTTTTTRAR 172

RESULT 4
ID Q4SDD4_TETNG PRELIMINARY; PRT; 1139 AA.
AC Q4SDD4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 3 SCAF14639, whole genome shotgun sequence.
GN ORFNames=GSTENG0002093001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01014639; CAG01348.1; -; Genomic DNA.
SQ SEQUENCE 1139 AA; 121432 MW; 7E2BD59621B51FCC CRC64;

Query Match 100.0%; Score 20; DB 2; Length 1139;
Best Local Similarity 33.3%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXRXR 14
DB 161 RRSSTTTTTRAR 172

RESULT 5
ID Q74EX0_GEOSL PRELIMINARY; PRT; 194 AA.
AC Q74EX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=GSU0839;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Mehe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden J.T., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA "Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR34169.1; -; Genomic_DNA.
DR TIGR; GSU0839; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 194 AA; 21055 MW; D0B0D918D3F2CACB CRC64;

Query Match 95.0%; Score 19; DB 2; Length 194;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 139 RRSSSSLRTR 150

RESULT 6
QYF0M2 Oryza PRELIMINARY; PRT; 214 AA.
AC QYF0M2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein P0450A04.111.
GN Name=P0450A04.111;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0450A04.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004274; BAC83398.1; -; Genomic_DNA.
DR Gramene; QYF0M2; -.
KW Hypothetical protein.
SQ SEQUENCE 214 AA; 23349 MW; E106D482D50E50C0 CRC64;

Query Match 95.0%; Score 19; DB 2; Length 214;
Best Local Similarity 33.3%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 16 RRSSSSSRRSR 27

RESULT 7
Q4LNR3 9BURK PRELIMINARY; PRT; 444 AA.
AC Q4LNR3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Delta 1-pyrroline-5-carboxylate reductase (EC 1.5.1.2).
GN ORFNames=Bcen2424DRAFT_2557;
OS Burkholderia cenocepacia H12424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331272;

```

```

RN NUCLEOTIDE SEQUENCE.
RP STRAIN=H12424;
RC US DOE Joint Genome Institute (JGI-PGF);
RG Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHL01000036; EAM17718.1; -; Genomic_DNA.
KW Oxidoreductase.
SQ SEQUENCE 444 AA; 47128 MW; 6219556CF63899C7 CRC64;

Query Match 95.0%; Score 19; DB 2; Length 444;
Best Local Similarity 33.3%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 96 RRATRAASRTAR 107

RESULT 8
AMPA SYNEL STANDARD; PRT; 497 AA.
AC Q8DI46;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
DE (LAP) (Leucyl aminopeptidase).
GN Name=pepa; OrderedLocusNames=tlr1745;
OS Synecococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32046;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpso S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
CC -! FUNCTION: Presumably involved in the processing and regular
CC turnover of intracellular proteins. Catalyzes the removal of
CC unsubstituted N-terminal amino acids from various peptides (By
CC similarity).
CC -! CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
CC Yaa-, in which Xaa is preferably Leu, but may be other amino acids
CC including Pro although not Arg or Lys, and Yaa may be Pro. Amino
CC acid amides and methyl esters are also readily hydrolyzed, but
CC rates on arylamides are exceedingly low.
CC -! COFACTOR: Binds 2 manganese ions per subunit (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -! SIMILARITY: Belongs to the peptidase M17 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```


CC use as long as its content is in no way modified and this statement is not removed.

CC -----
CC EMBL; BA000039; BAC09297.1; -, Genomic_DNA.

CC HSSP; P00727; ILAM.

CC MEROPS; M17.002; -.

CC HAMAP; MF_00181; -, 1.

CC InterPro; IPR011356; Peptidase_M17.

CC InterPro; IPR00819; Peptidase_M17_C.

CC Pfam; PF00883; Peptidase_M17_N.

CC Pfam; PF02789; Peptidase_M17; 1.

CC Pfam; PF02789; Peptidase_M17_N; 1.

CC PIRSF; PIRSF001116; Ctel_ammptase; 1.

CC PRINTS; PR00481; LAMNOPPTASE.

CC PROSITE; PS00631; Cytosol_AP; 1.

CC AminoPeptidase; Complete proteome; Hydrolase; Manganese;

CC Metal-binding; Protease.

CC ACT_SITE 276 276 Potential.

CC ACT_SITE 351 351 Potential.

CC METAL 264 264 Manganese 2 (By similarity).

CC METAL 269 269 Manganese 1 and 2 (By similarity).

CC METAL 287 287 Manganese 2 (By similarity).

CC METAL 347 347 Manganese 1 (By similarity).

CC METAL 349 349 Manganese 1 and 2 (By similarity).

CC SEQUENCE 497 AA; 53090 MW; B99C8D4B015B0411 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 497;

Best Local Similarity 33.3%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14

DB 93 RTAAATARTAR 104

RESULT 9

PERQ1 HUMAN STANDARD; PRT; 817 AA.

ID PERQ1 HUMAN STANDARD; PRT; 817 AA.

AC O75420;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE PERQ amino acid rich with GYF domain protein 1.

GN Name=PERQ1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RX MEDLINE=99018118; PubMed=9799793;

RA Gloeckner G., Scherter S., Schattevoy R., Boright A.P., Weber J.,

RA Tsui L.-C., Rosenthal A.;

RT "Large-scale sequencing of two regions in human chromosome 7q22:

RT reveals 17 genes.";

RL Genome Res. 8:1060-1073 (1998).

CC -1- SIMILARITY: Contains 1 GYF domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC EMBL; AF053356; AAC78792.1; -, Genomic_DNA.

CC Ensembl; ENSG00000146830; Homo sapiens.

CC HGNC; HGNC:9126; PERQ1.

CC InterPro; IPR003169; GYF.

CC Pfam; PF02213; GYF; 1.

CC SMART; SM00444; GYF; 1.

CC PROSITE; PS50829; GYF; 1.

FT DOMAIN 352 400 GYF.

FT COMPIAS 113 120 Poly-Glu.

FT COMPIAS 176 181 Poly-Gly.

FT COMPIAS 256 260 Poly-Glu.

FT COMPIAS 426 495 Gln-rich.

FT COMPIAS 474 480 Poly-Pro.

FT COMPIAS 481 486 Poly-Gln.

FT COMPIAS 751 757 Poly-Gln.

SQ SEQUENCE 817 AA; 89741 MW; C727AD2E7C2E2581 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 817;

Best Local Similarity 33.3%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14

DB 523 RRSAASSRRSR 534

RESULT 10

Q4QE71_LEIMA PRELIMINARY; PRT; 833 AA.

ID Q4QE71_LEIMA PRELIMINARY; PRT; 833 AA.

AC Q4QE71;

DT 13-SEP-2005 (T-EMBLrel. 31, Created)

DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=LmjF17.1200;

OS Leishmania major.

OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID=5664;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Friedlin;

RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,

RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,

RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; CT005256; CAJ03930.1; -, Genomic_DNA.

KW Hypothetical protein.

SQ SEQUENCE 833 AA; 87127 MW; 7F8BD43D0F4C2256 CRC64;

Query Match 95.0%; Score 19; DB 2; Length 833;

Best Local Similarity 33.3%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14

DB 653 RRTSSSSLSRSAR 664

RESULT 11

Q4NSL6_9DELIT PRELIMINARY; PRT; 856 AA.

ID Q4NSL6_9DELIT PRELIMINARY; PRT; 856 AA.

AC Q4NSL6;

DT 13-SEP-2005 (T-EMBLrel. 31, Created)

DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=AdehDRAFT_1669;

OS Anaeromyxobacter dehalogenans 2CP-C.

OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;

OC Cytophactereae; Myxococcaceae; Anaeromyxobacter.

OX NCBI_TaxID=290397;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=2CP-C;

RG US DOE Joint Genome Institute (JGI-PGF);

RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,

RA Hammon N., Israni S., Pitluck S., Richardson P.;

RT "Sequencing of the draft genome assembly of Anaeromyxobacter

RT dehalogenans 2CP-C.";

RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.


```

[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN-2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAHD01000021; EAL78630.1; -; Genomic_DNA.
DR HYPOTHETICAL PROTEIN.
KW SEQUENCE 856 AA; 89899 MW; F33C3D7D3B663665 CRC64;
SQ

Query Match 95.0%; Score 19; DB 2; Length 856;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 738 RRSAAASRRR 749

RESULT 12
Q5N831_ORYSA PRELIMINARY; PRT; 57 AA.
ID Q5N831;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein B1099D03.55.
GN Name=B1099D03.55;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa M., Katagiri S., Kikuta A., Kobayashi T., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shinokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003431; BAD82385.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 57 AA; 6587 MW; 7A9814F81F280924 CRC64;

Query Match 90.0%; Score 18; DB 2; Length 57;
Best Local Similarity 33.3%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 40 RRTDSALARSAR 51

RESULT 13
SP4_XENLA
ID SP4_XENLA PRT; 78 AA.
AC P24056;

DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sperm-specific basic nuclear protein SP4.
GN Name=SP4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-43 AND 64-78.
RC TISSUE=Round spermatid;
RX MEDLINE=91200205; PubMed=2015853;
RA Hiroyoshi H., Uno S., Yokota T., Katagiri C., Nishida H., Takai M.,
RA Agata K., Eguchi G., Abe S.-I.;
RT "Isolation of cDNA for a Xenopus sperm-specific basic nuclear protein
RT (SP4) and evidence for expression of SP4 mRNA in primary
RT spermatocytes.";
RL Exp. Cell Res. 194:95-99(1991).
CC -!- DEVELOPMENTAL STAGE: SP4 gene is transcribed in or before primary
CC spermatocyte stage but is translated at the round spermatid stage.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; D00916; BAA00762.1; -; mRNA.
DR PIR; JH0404; JH0404.
KW Direct protein sequencing; Nuclear protein; Repeat; Sperm.
FT INIT_MET 0
FT REPEAT 44 51
FT REPEAT 52 59
FT REPEAT 78 AA; 9194 MW; B342CD9CB8FD2FBA CRC64;
SQ SEQUENCE 78 AA; 9194 MW; B342CD9CB8FD2FBA CRC64;

Query Match 90.0%; Score 18; DB 1; Length 78;
Best Local Similarity 33.3%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 44 RRARTSTARRAR 55

RESULT 14
Q53X49_XENLA PRELIMINARY; PRT; 79 AA.
ID Q53X49_XENLA PRELIMINARY;
AC Q53X49;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Sperm-specific nuclear basic protein (SP4).
GN Name=XLSP43; Synonyms=XLSP42, XLSP44;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=J;
RX MEDLINE=96125743; PubMed=8541323; DOI=10.1016/0304-4165(95)00124-7;
RT Mita K., Ariyoshi N., Abe S., Takamune K., Katagiri C.;
RT "Structure of genes for sperm-specific nuclear basic protein (SP4) in
RT Xenopus laevis.";
RL Biochim. Biophys. Acta 1245:430-438(1995).
DR EMBL; D45253; BAA08210.1; -; Genomic_DNA.
DR EMBL; D45253; BAA08211.1; -; Genomic_DNA.
DR EMBL; D45253; BAA08209.1; -; Genomic_DNA.
SQ SEQUENCE 79 AA; 9325 MW; 920C021D88FD70DC CRC64;
```

Query Match 90.0%; Score 18; DB 2; Length 79;
Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
Db 45 RRARTSTARRAR 56

RESULT 15

O6XN62 RHOER
ID Q6XN62 RHOER PRELIMINARY; PRT; 85 AA.
AC O6XN62;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
DE ORFNames=PBD2.084;
OS Rhodococcus erythropolis.
OC Plasmid pBD2.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=1833;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BD2;
RX MEDLINE=22803265; PubMed=12933100;
RX DOI=10.1128/JB.185.17.5269-5274.2003;
RA Stecker C., Johann A., Herzberg C., Averhoff B., Gottschalk G.;
RT "Complete nucleotide sequence and genetic organization of the 210-
RT kilobase linear plasmid of Rhodococcus erythropolis BD2.";
RL J. Bacteriol. 185:5269-5274(2003).
DR EMBL; AY223810; AAP73969.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 85 AA; 9111 MW; BE17D81E56DD0A2A CRC64;

Query Match 90.0%; Score 18; DB 2; Length 85;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
Db 14 RRTTTSVRAVR 25

Search completed: March 29, 2006, 01:49:13
Job time : 131.062 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 01:49:32 ; Search time 29.3125 Seconds
(without alignments)
39.487 Million cell updates/sec

Title: US-10-712-447-210

Perfect score: 20

Sequence: 1 XXRRXXXXXXRXR 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCUTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	95.0	133	2	US-09-252-991A-21845 Sequence 21845, A
2	19	95.0	189	2	US-09-252-991A-32376 Sequence 32376, A
3	19	95.0	442	2	US-09-252-991A-23285 Sequence 23285, A
4	18	90.0	16	1	US-08-660-592-11 Sequence 11, Appl
5	18	90.0	16	2	US-09-166-930A-8 Sequence 8, Appl
6	18	90.0	16	2	US-09-905-691-4 Sequence 4, Appl
7	18	90.0	16	2	US-09-905-691-5 Sequence 5, Appl
8	18	90.0	19	1	US-08-660-592-10 Sequence 10, Appl
9	18	90.0	19	2	US-09-905-691-2 Sequence 2, Appl
10	18	90.0	103	2	US-09-252-991A-32536 Sequence 32536, A
11	18	90.0	113	2	US-09-252-991A-17175 Sequence 17175, A
12	18	90.0	134	2	US-09-252-991A-21251 Sequence 21251, A
13	18	90.0	139	2	US-09-252-991A-24681 Sequence 24681, A
14	18	90.0	139	2	US-09-252-991A-26906 Sequence 26906, A
15	18	90.0	141	2	US-09-252-991A-23676 Sequence 23676, A
16	18	90.0	142	2	US-09-252-991A-31446 Sequence 31446, A
17	18	90.0	152	2	US-09-252-991A-25319 Sequence 25319, A
18	18	90.0	207	2	US-09-252-991A-21774 Sequence 21774, A
19	18	90.0	208	2	US-09-252-991A-17638 Sequence 17638, A
20	18	90.0	209	2	US-09-252-991A-21363 Sequence 21363, A
21	18	90.0	231	2	US-09-252-991A-17218 Sequence 17218, A
22	18	90.0	237	2	US-09-252-991A-32341 Sequence 32341, A
23	18	90.0	263	2	US-09-252-991A-19961 Sequence 19961, A
24	18	90.0	277	2	US-09-252-991A-28460 Sequence 28460, A
25	18	90.0	282	2	US-09-252-991A-29124 Sequence 29124, A
26	18	90.0	296	2	US-09-252-991A-20067 Sequence 20067, A
27	18	90.0	296	2	US-09-252-991A-32162 Sequence 32162, A

ALIGNMENTS

RESULT 1

US-09-252-991A-21845
; Sequence 21845, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21845
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21845

Query Match 95.0%; Score 19; DB 2; Length 133;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
|||
Db 22 RRSARTSTRATR 33

RESULT 2

US-09-252-991A-32376
; Sequence 32376, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32376
; LENGTH: 189
; TYPE: PRT

```
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23276

Query Match          95.0%; Score 19; DB 2; Length 189;
Best Local Similarity 33.3%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
Db 34 RRTSASARRASR 45

RESULT 3
US-09-252-991A-23285
; Sequence 23285, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23285
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23285

Query Match          95.0%; Score 19; DB 2; Length 442;
Best Local Similarity 33.3%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
Db 307 RRAASRSRRTAR 318

RESULT 4
US-08-660-592-11
; Sequence 11, Application US/08660592
; Patent No. 5877153
; GENERAL INFORMATION:
; APPLICANT: HARRIS, Robert B.
; APPLICANT: SOBEL, Michael
; TITLE OF INVENTION: NOVEL HEPARIN BINDING PEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,592
; FILING DATE: 11-JUN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 006338-001
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-592-11

Query Match          90.0%; Score 18; DB 1; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
Db 2 RRAAARAARRAR 13

RESULT 5
US-09-166-930A-8
; Sequence 8, Application US/09166930A
; Patent No. 6200955
; GENERAL INFORMATION:
; APPLICANT: HARRIS, Robert B.
; APPLICANT: SOBEL, Michael
; TITLE OF INVENTION: NOVEL HEPARIN BINDING PEPTIDES
; FILE REFERENCE: 006338-006
; CURRENT APPLICATION NUMBER: US/09/166,930A
; CURRENT FILING DATE: 1998-10-06
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: US 08/660,592
; PRIOR FILING DATE: 1996-06-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Tris Arg #3
US-09-166-930A-8

Query Match          90.0%; Score 18; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
Db 2 RRAAARAARRAR 13

RESULT 6
US-09-905-691-4
; Sequence 4, Application US/09905691
; Patent No. 6756206
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological
; FILE REFERENCE: 006338-017
; CURRENT APPLICATION NUMBER: US/09/905,691
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tris-Arginine Helix #3
```

US-09-905-691-4

Query Match 90.0%; Score 18; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
Db 2 RRAAARARR 13

RESULT 7

US-09-905-691-5
Sequence 5, Application US/09905691

Patent No. 6756206

GENERAL INFORMATION:

APPLICANT: Harris, Robert B.

APPLICANT: Wolz, Russell L.

APPLICANT: Wolz, Gabriella

TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological

TITLE OF INVENTION: Fluids Using Cationic Helix Peptides

FILE REFERENCE: 006338-017

CURRENT APPLICATION NUMBER: US/09/905,691

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Tris-Arginine Helix #3

US-09-905-691-5

Query Match 90.0%; Score 18; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
Db 2 RRAAARARR 13

RESULT 8

US-08-660-592-10
Sequence 10, Application US/08660592

Patent No. 6871153

GENERAL INFORMATION:

APPLICANT: Harris, Robert B.

APPLICANT: Sobel, Michael

TITLE OF INVENTION: NOVEL HEPARIN BINDING PEPTIDES

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSER: BURNS, DOANE, SWECKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,592

FILING DATE: 11-JUN-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: McGowan, Malcolm K.

REGISTRATION NUMBER: 39,300

REFERENCE/DOCKET NUMBER: 006338-001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-660-592-10

Query Match 90.0%; Score 18; DB 1; Length 19;

Best Local Similarity 33.3%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
Db 5 RRAAARARR 16

RESULT 9

US-09-905-691-2

Sequence 2, Application US/09905691

Patent No. 6756206

GENERAL INFORMATION:

APPLICANT: Harris, Robert B.

APPLICANT: Wolz, Russell L.

APPLICANT: Wolz, Gabriella

TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological

TITLE OF INVENTION: Fluids Using Cationic Helix Peptides

FILE REFERENCE: 006338-017

CURRENT APPLICATION NUMBER: US/09/905,691

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Bis-Arginine Helix #2

US-09-905-691-2

Query Match 90.0%; Score 18; DB 2; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
Db 5 RRAAARARR 16

RESULT 10

US-09-252-991A-32536

Sequence 32536, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32536

LENGTH: 103

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32536

```
Query Match          90.0%; Score 18; DB 2; Length 103;
Best Local Similarity 33.3%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
   |||||
Db 56 RRPSSATARRSR 67

RESULT 11
US-09-252-991A-17175
; Sequence 17175, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17175
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17175

Query Match          90.0%; Score 18; DB 2; Length 113;
Best Local Similarity 33.3%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
   |||||
Db 84 RRSACASSRAB 95

RESULT 12
US-09-252-991A-21251
; Sequence 21251, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21251
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21251

Query Match          90.0%; Score 18; DB 2; Length 134;
Best Local Similarity 33.3%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
   |||||
Db 107 RRAARSASRAGR 118

RESULT 13
```

```
US-09-252-991A-24681
; Sequence 24681, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24681
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24681

Query Match          90.0%; Score 18; DB 2; Length 139;
Best Local Similarity 33.3%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
   |||||
Db 16 RRSAGRRSSR 27

RESULT 14
US-09-252-991A-26906
; Sequence 26906, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26906
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26906

Query Match          90.0%; Score 18; DB 2; Length 139;
Best Local Similarity 33.3%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
   |||||
Db 124 RRAARSARTAR 135

RESULT 15
US-09-252-991A-23676
; Sequence 23676, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
```

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23676
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23676

Query Match 90.0%; Score 18; DB 2; Length 141;
Best Local Similarity 33.3%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 95 RRSADRSARSAR 106

Search completed: March 29, 2006, 01:51:16
Job time : 30.3125 secs

This Page Blank (usptn)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 02:05:02 ; Search time 119 Seconds
(without alignments)
49.156 Million cell updates/sec

Title: US-10-712-447-210

Perfect score: 20

Sequence: 1 XXXRXXXXXXRXR 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	95.0	323	4	US-10-425-114-59856 Sequence 59856, A
2	19	95.0	533	4	US-10-085-198-124 Sequence 124, App
3	19	95.0	712	4	US-10-437-963-162715 Sequence 162715,
4	19	95.0	19725	4	US-10-084-846A-4 Sequence 4, Appli
5	18	90.0	16	3	US-09-905-691-4 Sequence 4, Appli
6	18	90.0	16	3	US-09-905-691-5 Sequence 5, Appli
7	18	90.0	19	3	US-09-905-691-2 Sequence 2, Appli
8	18	90.0	64	4	US-10-425-114-45271 Sequence 45271, A
9	18	90.0	87	4	US-10-437-963-184083 Sequence 184083,
10	18	90.0	118	4	US-10-425-115-325436 Sequence 325436,
11	18	90.0	120	4	US-10-437-963-104880 Sequence 104880,
12	18	90.0	124	4	US-10-425-115-286800 Sequence 286800,
13	18	90.0	127	3	US-09-764-847-886 Sequence 886, App
14	18	90.0	127	3	US-09-154-886 Sequence 118401,
15	18	90.0	134	4	US-10-437-963-118401 Sequence 118401,
16	18	90.0	136	4	US-10-425-114-50352 Sequence 50352, A
17	18	90.0	140	4	US-10-425-114-48089 Sequence 48089, A
18	18	90.0	140	4	US-10-437-963-113409 Sequence 113409,
19	18	90.0	149	4	US-10-437-963-156048 Sequence 156048,
20	18	90.0	173	4	US-10-437-963-197400 Sequence 197400,
21	18	90.0	190	4	US-10-425-114-56334 Sequence 56334, A
22	18	90.0	193	4	US-10-437-963-194450 Sequence 194450,
23	18	90.0	211	4	US-10-425-115-198672 Sequence 198672,
24	18	90.0	216	4	US-10-437-963-135886 Sequence 135886,
25	18	90.0	226	4	US-10-156-761-14245 Sequence 14245, A
26	18	90.0	245	3	US-09-738-626-3948 Sequence 3948, Ap
27	18	90.0	255	4	US-10-425-114-67642 Sequence 67642, A

28	18	90.0	255	4	US-10-437-963-194527 Sequence 194527,
29	18	90.0	272	4	US-10-437-963-150101 Sequence 150101,
30	18	90.0	281	4	US-10-425-114-46297 Sequence 46297, A
31	18	90.0	325	4	US-10-425-114-72973 Sequence 72973, A
32	18	90.0	357	4	US-10-282-122A-50703 Sequence 50703, A
33	18	90.0	403	4	US-10-437-963-168937 Sequence 168937,
34	18	90.0	437	4	US-10-437-963-125004 Sequence 125004,
35	18	90.0	19608	4	US-10-084-846A-8 Sequence 8, Appli
36	18	90.0	19695	4	US-10-084-846A-3 Sequence 3, Appli
37	17	85.0	36	4	US-10-050-704-210 Sequence 210, App
38	17	85.0	36	4	US-10-798-512-210 Sequence 55011, A
39	17	85.0	36	4	US-10-767-701-55011 Sequence 37, Appli
40	17	85.0	45	3	US-09-912-962-37 Sequence 32306, A
41	17	85.0	46	4	US-10-029-386-32306 Sequence 147658,
42	17	85.0	55	4	US-10-437-963-147658 Sequence 350524,
43	17	85.0	57	4	US-10-425-115-350524 Sequence 338158,
44	17	85.0	58	4	US-10-425-115-338158 Sequence 173763,
45	17	85.0	59	4	US-10-424-599-173763 Sequence 173763,

ALIGNMENTS

RESULT 1

US-10-425-114-59856
; Sequence 59856, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59856
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3732-012-E4_FLI.pep
US-10-425-114-59856

Query Match 95.0%; Score 19; DB 4; Length 323;
Best Local Similarity 33.3%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 270 RRSAAASRTAR 281

RESULT 2

US-10-085-198-124
; Sequence 124, Application US/10085198
; Publication No. US2004000907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-124

Query Match 95.0%; Score 19; DB 4; Length 533;
Best Local Similarity 33.3%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 56 RRAAATSRAR 67

RESULT 3

US-10-437-963-162715
; Sequence 162715, Application US/10437963
; Publication No. US2004012334A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162715
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61780C.1.pep
US-10-437-963-162715

Query Match 95.0%; Score 19; DB 4; Length 712;
Best Local Similarity 33.3%; Pred. No. 4.2e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 321 RRLASAAARAR 332

RESULT 4

US-10-084-846A-4
; Sequence 4, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological

; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLERWEG, AGNES
; APPLICANT: TREFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 19725
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
US-10-084-846A-4

Query Match 95.0%; Score 19; DB 4; Length 19725;
Best Local Similarity 33.3%; Pred. No. 6.1e+04;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 11142 RRRSTASRTSR 11153

RESULT 5

US-09-905-691-4
; Sequence 4, Application US/09905691
; Publication No. US20020164329A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological
; TITLE OF INVENTION: Fluids Using Cationic Helix Peptides
; FILE REFERENCE: 006338-017
; CURRENT APPLICATION NUMBER: US/09/905,691
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tris-Arginine Helix #3
US-09-905-691-4

Query Match 90.0%; Score 18; DB 3; Length 16;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 2 RRAAARAR 13

RESULT 6

US-09-905-691-5
; Sequence 5, Application US/09905691
; Publication No. US20020164329A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological

; TITLE OF INVENTION: Fluids Using Cationic Helix Peptides
; FILE REFERENCE: 006338-017
; CURRENT APPLICATION NUMBER: US/09/905,691
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tris-Arginine Helix #3
US-09-905-691-5

Query Match 90.0%; Score 18; DB 3; Length 16;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
|||
DB 2 RRAAARAARR 13

RESULT 7
US-09-905-691-2
; Sequence 2, Application US/09905691
; Publication No. US20020164329A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological
; TITLE OF INVENTION: Fluids Using Cationic Helix Peptides
; FILE REFERENCE: 006338-017
; CURRENT APPLICATION NUMBER: US/09/905,691
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bis-Arginine Helix #2
US-09-905-691-2

Query Match 90.0%; Score 18; DB 3; Length 19;
Best Local Similarity 33.3%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
|||
DB 5 RRAAARAARR 16

RESULT 8
US-10-425-114-45271
; Sequence 45271, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45271

; LENGTH: 64
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700431372_FLI.pep
US-10-425-114-45271

Query Match 90.0%; Score 18; DB 4; Length 64;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
|||
DB 19 RRTSSRTRATR 30

RESULT 9
US-10-437-963-184083
; Sequence 184083, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 184083
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8110C.1.pep
US-10-437-963-184083

Query Match 90.0%; Score 18; DB 4; Length 87;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
|||
DB 61 RRRSTRASRSR 72

RESULT 10
US-10-425-115-325436
; Sequence 325436, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 325436
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_59869C.1.pep

US-10-425-115-325436

Query Match 90.0%; Score 18; DB 4; Length 118;
Best Local Similarity 33.3%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
|||
Db 17 RRATAVSSRRTR 28

RESULT 11

US-10-437-963-104880
; Sequence 104880, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 104880
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(120)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102172C.1.pep
US-10-437-963-104880

Query Match 90.0%; Score 18; DB 4; Length 120;
Best Local Similarity 33.3%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
|||
Db 56 RRSATAKQTR 67

RESULT 12

US-10-425-115-286800
; Sequence 286800, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286800
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(124)

; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_24656C.1.pep
US-10-425-115-286800

Query Match 90.0%; Score 18; DB 4; Length 124;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
|||
Db 48 RRKAASRTRSSR 59

RESULT 13

US-09-764-847-886
; Sequence 886, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; Prior application data removed - consult PALM or file wrapper
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 886
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (76)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (85)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (88)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (94)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (108)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (111)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-847-886

Query Match 90.0%; Score 18; DB 3; Length 127;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
|||
Db 59 RRATSTARAIR 70

RESULT 14
US-10-092-154-886
; Sequence 886, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154

;; CURRENT FILING DATE: 2002-03-07
;; NUMBER OF SEQ ID NOS: 2003
;; Prior Application removed - See File Wrapper or Palm
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 886
;; LENGTH: 127
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (76)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: misc_feature
;; LOCATION: (84)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: misc_feature
;; LOCATION: (85)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: misc_feature
;; LOCATION: (88)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: misc_feature
;; LOCATION: (94)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: misc_feature
;; LOCATION: (108)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: misc_feature
;; LOCATION: (111)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-092-154-886

Best Local Similarity 33.3%; Pred. No. 2e+03; Mismatches 0; Indels 8; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 8; Gaps 0;
Qy 3 RRRXXXXXXR 14
Db 81 RRRATATRAAR 92

Search completed: March 29, 2006, 02:10:40
Job time : 120 secs

Query Match 90.0%; Score 18; DB 4; Length 127;
Best Local Similarity 33.3%; Pred. No. 1.9e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRRXXXXXXR 14
Db 59 RRRATATRAAR 70

RESULT 15
US-10-437-963-118401
; Sequence 118401, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118401
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(134)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_21716C.1.pap
US-10-437-963-118401

Query Match 90.0%; Score 18; DB 4; Length 134;

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 02:06:17 ; Search time 13.125 Seconds
(without alignments)
31.461 Million cell updates/sec

Title: US-10-712-447-210
Perfect score: 20
Sequence: 1 XRRXXXXXXXXR 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pap:
2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pap:
3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pap:
4: /SIDSS/ptodata/1/pubpaa/PCR_NEW PUB.pap:
5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pap:
6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pap:
7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pap:
8: /SIDSS/ptodata/1/pubpaa/US60_NEW PUB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	95.0	141	7	US-11-096-568A-4518
2	18	90.0	101	7	US-11-096-568A-25321
3	18	90.0	341	7	US-11-096-568A-27148
4	18	90.0	496	7	US-11-182-016-33
5	17	85.0	32	7	US-11-078-469-34
6	17	85.0	32	7	US-11-078-469-71
7	17	85.0	173	7	US-11-087-099-10728
8	17	85.0	189	7	US-11-096-568A-20087
9	17	85.0	192	7	US-11-096-568A-19930
10	17	85.0	200	7	US-11-096-568A-16604
11	17	85.0	211	7	US-11-087-099-6884
12	17	85.0	212	7	US-11-096-568A-20086
13	17	85.0	274	6	US-10-821-234-956
14	17	85.0	274	7	US-11-096-568A-22603
15	17	85.0	277	7	US-11-096-568A-19929
16	17	85.0	300	7	US-11-096-568A-27037
17	17	85.0	319	7	US-11-096-568A-24347
18	17	85.0	536	7	US-11-087-099-9046
19	17	85.0	2597	7	US-11-124-367A-466
20	17	85.0	2597	7	US-11-124-367A-468
21	17	85.0	3012	7	US-11-124-367A-465
22	17	85.0	3144	7	US-11-055-035-1
23	16	80.0	26	7	US-11-078-256-308
24	16	80.0	87	7	US-11-166-609-16
25	16	80.0	95	7	US-11-096-568A-25670

RESULT 1
US-11-096-568A-4518
; Sequence 4518, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 4518
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)..(141)
; OTHER INFORMATION: Ceres Seq. ID no. 13638657
US-11-096-568A-4518

Query Match 95.0%; Score 19; DB 7; Length 141;
Best Local Similarity 33.3%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRRXXXXXXXXR 14
Db 28 RRRSTTRRRR 39

RESULT 2
US-11-096-568A-25321
; Sequence 25321, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25321
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:

Sequence 13882, A
Sequence 7047, Ap
Sequence 14539, A
Sequence 22510, A
Sequence 14218, A
Sequence 22509, A
Sequence 9617, Ap
Sequence 26671, A
Sequence 18247, A
Sequence 7046, Ap
Sequence 1290, Ap
Sequence 7045, Ap
Sequence 18246, A
Sequence 1876, Ap
Sequence 5420, Ap
Sequence 18556, A
Sequence 18555, A
Sequence 24229, A
Sequence 24216, A
Sequence 1598, Ap

; NAME/KEY: misc feature
; LOCATION: (1)..(101)
; OTHER INFORMATION: Ceres Seq. ID no. 13580080
US-11-096-568A-25321

Query Match 90.0%; Score 18; DB 7; Length 101;
Best Local Similarity 33.3%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 22 RRIATGAARSTR 33

RESULT 3

US-11-096-568A-27148
; Sequence 27148, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thetby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27148
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(341)
; OTHER INFORMATION: Ceres Seq. ID no. 15175533
US-11-096-568A-27148

Query Match 90.0%; Score 18; DB 7; Length 341;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 82 RRASSRRARASR 93

RESULT 4

US-11-182-016-33
; Sequence 33, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tks 118
US-11-182-016-33

Query Match 90.0%; Score 18; DB 7; Length 496;
Best Local Similarity 33.3%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||

Db 273 RRAASRSRSRR 284

RESULT 5

US-11-078-469-34
; Sequence 34, Application US/11078469
; Publication No. US20050282755A1
; GENERAL INFORMATION:
; APPLICANT: HART, SCOTT A.
; APPLICANT: ZEH, KARIN
; APPLICANT: MACHLEIDT, THOMAS
; APPLICANT: STOLOW, DAVID
; APPLICANT: CONGER, DEE
; TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ANS-2001-UT
; CURRENT APPLICATION NUMBER: US/11/078,469
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 60/554,526
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 60/618,948
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 34
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide moiety
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-
; OTHER INFORMATION: H2N-Arg
US-11-078-469-34

Query Match 85.0%; Score 17; DB 7; Length 32;
Best Local Similarity 33.3%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 3 RRAATRVSTGR 14

RESULT 6

US-11-078-469-71
; Sequence 71, Application US/11078469
; Publication No. US20050282755A1
; GENERAL INFORMATION:
; APPLICANT: HART, SCOTT A.
; APPLICANT: ZEH, KARIN
; APPLICANT: MACHLEIDT, THOMAS
; APPLICANT: STOLOW, DAVID
; APPLICANT: CONGER, DEE
; TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ANS-2001-UT
; CURRENT APPLICATION NUMBER: US/11/078,469
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 60/554,526
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 60/618,948
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 71
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide moiety
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)_RES
; OTHER INFORMATION: H2N-Arg
US-11-078-469-71

Query Match 85.0%; Score 17; DB 7; Length 32;
Best Local Similarity 33.3%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
|||
Db 3 RRAATRVARTGR 14

RESULT 7
US-11-087-099-10728
; Sequence 10728, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10728
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(173)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-10728

Query Match 85.0%; Score 17; DB 7; Length 173;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
|||
Db 15 RRAATSRRAAR 26

RESULT 8
US-11-096-568A-20087
; Sequence 20087, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20087
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(189)
; OTHER INFORMATION: Ceres Seq. ID no. 12376847
US-11-096-568A-20087

Query Match 85.0%; Score 17; DB 7; Length 189;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14

Db 147 RRSARKTRRSAR 158
|||

RESULT 9
US-11-096-568A-19930
; Sequence 19930, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19930
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(192)
; OTHER INFORMATION: Ceres Seq. ID no. 12375688
US-11-096-568A-19930

Query Match 85.0%; Score 17; DB 7; Length 192;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
|||
Db 63 RRAAASGREER 74

RESULT 10
US-11-096-568A-16604
; Sequence 16604, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 16604
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(200)
; OTHER INFORMATION: Ceres Seq. ID no. 12353107
US-11-096-568A-16604

Query Match 85.0%; Score 17; DB 7; Length 200;
Best Local Similarity 33.3%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
|||
Db 170 RRAAARGR 181

RESULT 11
US-11-087-099-6884
; Sequence 6884, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6884
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Zea mays
US-11-087-099-6884

Query Match 85.0%; Score 17; DB 7; Length 211;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 178 RRAAKAARAR 189

RESULT 12
US-11-096-568A-20086
; Sequence 20086, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20086
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(212)
; OTHER INFORMATION: Ceres Seq. ID no. 12376846
US-11-096-568A-20086

Query Match 85.0%; Score 17; DB 7; Length 212;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 170 RRSARKTRRSAR 181

RESULT 13
US-10-821-234-956
; Sequence 956, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 956
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-956

Query Match 85.0%; Score 17; DB 6; Length 274;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 205 RRSRSASLRRSR 216

RESULT 14
US-11-096-568A-22603
; Sequence 22603, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22603
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(274)
; OTHER INFORMATION: Ceres Seq. ID no. 12409336
US-11-096-568A-22603

Query Match 85.0%; Score 17; DB 7; Length 274;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 217 RRSRAARRRSR 228

RESULT 15
US-11-096-568A-19929
; Sequence 19929, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19929
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(277)
; OTHER INFORMATION: Ceres Seq. ID no. 12375687
US-11-096-568A-19929

Query Match 85.0%; Score 17; DB 7; Length 277;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 148 RRAAASGREER 159

Search completed: March 29, 2006, 02:11:17
Job time : 14.125 secs

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 01:38:52 ; Search time 159.75 Seconds
(without alignments)
49.507 Million cell updates/sec

Title: US-10-712-447-5

Perfect score: 98

Sequence: 1 GIRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	ADO34231	Ado34231 Synthetic
2	98	100.0	18	ADO34225	Ado34225 Synthetic
3	98	100.0	18	ADO34228	Ado34228 Synthetic
4	98	100.0	18	ADO34236	Ado34236 Synthetic
5	98	100.0	18	ADO34233	Ado34233 Synthetic
6	95	96.9	18	ADO34314	Ado34314 Synthetic
7	94	95.9	18	ADO34354	Ado34354 Synthetic
8	94	95.9	18	ADO34338	Ado34338 Synthetic
9	94	95.9	18	ADO34352	Ado34352 Synthetic
10	94	95.9	18	ADO34340	Ado34340 Synthetic
11	94	95.9	18	ADO34339	Ado34339 Synthetic
12	92	93.9	18	ADO34297	Ado34297 Synthetic
13	92	93.9	18	ADO34244	Ado34244 Synthetic
14	92	93.9	18	ADO34276	Ado34276 Synthetic
15	90	91.8	18	ADO34227	Ado34227 Synthetic
16	90	91.8	18	ADO34350	Ado34350 Synthetic
17	89	90.8	18	ADO34322	Ado34322 Synthetic
18	88	89.8	18	ADO34336	Ado34336 Synthetic
19	88	89.8	18	ADO34335	Ado34335 Synthetic
20	88	89.8	18	ADO34337	Ado34337 Synthetic
21	88	89.8	18	ADO34241	Ado34241 Synthetic
22	87	88.8	18	ADO34240	Ado34240 Synthetic
23	86	87.8	18	ADO34284	Ado34284 Synthetic
24	86	87.8	18	ADO34305	Ado34305 Synthetic

25	85	86.7	18	ADO34239	Ado34239 Synthetic
26	85	86.7	18	ADO34344	Ado34344 Synthetic
27	85	86.7	18	ADO34319	Ado34319 Synthetic
28	84	85.7	18	ADO34245	Ado34245 Synthetic
29	84	85.7	18	ADO34301	Ado34301 Synthetic
30	84	85.7	18	ADO34343	Ado34343 Synthetic
31	84	85.7	18	ADO34318	Ado34318 Synthetic
32	82	83.7	18	ADO34302	Ado34302 Synthetic
33	82	83.7	18	ADO34279	Ado34279 Synthetic
34	82	83.7	18	ADO34303	Ado34303 Synthetic
35	82	83.7	18	ADO34242	Ado34242 Synthetic
36	82	83.7	18	ADO34300	Ado34300 Synthetic
37	82	83.7	18	ADO34281	Ado34281 Synthetic
38	82	83.7	18	ADO34317	Ado34317 Synthetic
39	81	82.7	18	ADO34323	Ado34323 Synthetic
40	81	82.7	18	ADO34280	Ado34280 Synthetic
41	80	81.6	18	ADO34264	Ado34264 Synthetic
42	79	80.6	18	ADO34320	Ado34320 Synthetic
43	78	79.6	18	AA18917	AA18917 Lecithin:
44	78	79.6	18	AA19171	AA19171 Lecithin:
45	78	79.6	18	RAY19425	RAY19425 Lecithin:

ALIGNMENTS

RESULT 1
ADO34231
ID ADO34231 standard; peptide; 18 AA.
XX
AC ADO34231;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.
XX
KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
KW vasotropic; antiarteriosclerotic; cerebroprotective; antilanginal;
KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
XX
OS Synthetic.
XX
PN WO2004043403-A2.
XX
PD 27-MAY-2004.
XX
PF 13-NOV-2003; 2003WO-US036268.
XX
PP 13-NOV-2002; 2002US-0425821P.
XX
PP (UABR-) UAB RES FOUND.
XX
PP Anantharamiah GM, Garber DW, Datta G;
XX
PP WPI; 2004-411629/38.
XX
PP Synthetic apolipoprotein-E mimicking polypeptide useful for treating
XX coronary artery disease, dysbetalipoproteinemia or atherosclerosis
XX comprises an amino acid sequence.
XX
PS Claim 4; SEQ ID NO 8; 79pp; English.
XX
CC The invention relates to a novel synthetic apolipoprotein-E mimicking
XX polypeptide. The invention further comprises an isolated nucleic acid
XX encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
XX a host cell, a recombinant cell or a transgenic, non-human subject
XX (including animal or plant) comprising the synthetic apolipoprotein-E
XX mimicking polypeptide encoding polynucleotide; a composition comprising
XX the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
XX an monoclonal antibody that specifically binds to the synthetic
XX apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipæmic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinæmia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;
 Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 2
 ADO34225
 ID ADO34225 standard; peptide; 18 AA.

XX AC ADO34225;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking polypeptide related R19L peptide.

XX KW apolipoprotein-E mimicking polypeptide; antilipæmic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinæmia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 18
 FT Modified-site 18 /note= "C-terminal amide"

XX WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 2; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipæmic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinæmia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 3

ADO34228
 ID ADO34228 standard; peptide; 18 AA.

XX AC ADO34228;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 5.

XX KW apolipoprotein-E mimicking polypeptide; antilipæmic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinæmia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 5; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 4
 ADO34236
 ID ADO34236 standard; peptide; 18 AA.

XX AC ADO34236;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiatic;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 13; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 5
 ADO34233

ID ADO34233 standard; peptide; 18 AA.

XX AC ADO34233;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiatic;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 10; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
 |||||
 Db 1 GIRFLGSIWRFIRAFVG 18
 |||||

RESULT 6
 ADO34314
 ID ADO34314 standard; peptide; 18 AA.
 AC ADO34314;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 91.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX
 OS Synthetic.
 XX
 PN WO2004043403-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036268.
 XX
 PR 13-NOV-2002; 2002US-0425821P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Anantharamiah GM, Garber DW, Datta G;
 XX
 DR WPI; 2004-411629/38.
 XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX
 PS Claim 4; SEQ ID NO 91; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 96.9%; Score 95; DB 8; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.8e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
 |||||
 Db 1 GIRFLGSIWRFIRAFVG 18
 |||||

RESULT 7
 ADO34354
 ID ADO34354 standard; peptide; 18 AA.
 XX
 AC ADO34354;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 131.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX
 OS Synthetic.
 XX
 PN WO2004043403-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036268.
 XX
 PR 13-NOV-2002; 2002US-0425821P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Anantharamiah GM, Garber DW, Datta G;
 XX
 DR WPI; 2004-411629/38.
 XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX
 PS Claim 4; SEQ ID NO 131; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of myocardial infarction or stroke; for breaking an embolus in the subject; and also for treating angina. The synthetic apolipoprotein-E mimicking polypeptide enhances binding of low-density lipoprotein (LDL) or very low density lipoprotein (VLDL) to a cell and enhances degradation of LDL or VLDL by a cell. This sequence represents a synthetic apolipoprotein-E mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRPIAFYVG 18

Db 1 GLRRFLGSIWRPIAFYVG 18

RESULT 8

ADO34338
ID ADO34338 standard; peptide; 18 AA.

XX AC ADO34338;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 115; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
CC polypeptide. The invention further comprises an isolated nucleic acid
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
CC a host cell, a recombinant cell or a transgenic, non-human subject
CC (including animal or plant) comprising the synthetic apolipoprotein-E
CC mimicking polypeptide encoding polynucleotide; a composition comprising
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
CC an monoclonal antibody that specifically binds to the synthetic
CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
CC mimicking polypeptide has the following activities: antilipemic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
CC useful for reducing serum cholesterol in a subject (including a mammal
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
CC chimpanzee or orangutan); for treating coronary artery disease,
CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
CC myocardial infarction or stroke; for breaking an embolus in the subject;
CC and also for treating angina. The synthetic apolipoprotein-E mimicking
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRPIAFYVG 18

Db 1 GLRRFLGSIWRPIAFYVG 18

RESULT 9

ADO34352
ID ADO34352 standard; peptide; 18 AA.

XX AC ADO34352;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 129; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
CC polypeptide. The invention further comprises an isolated nucleic acid
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
CC a host cell, a recombinant cell or a transgenic, non-human subject
CC (including animal or plant) comprising the synthetic apolipoprotein-E
CC mimicking polypeptide encoding polynucleotide; a composition comprising
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
CC an monoclonal antibody that specifically binds to the synthetic
CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
CC mimicking polypeptide has the following activities: antilipemic,
CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.5e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYG 18
 |||||:||||:||||
 Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 10
 ADO34340
 ID ADO34340 standard; peptide; 18 AA.

XX
 AC ADO34340;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiatic;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antiangular;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
 OS Synthetic.

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 PS WPI; 2004-411629/38.

XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 PS Claim 4; SEQ ID NO 117; 79pp; English.

XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.5e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYG 18
 |||||:||||:||||
 Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 11
 ADO34339

ID ADO34339 standard; peptide; 18 AA.

XX
 AC ADO34339;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiatic;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antiangular;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
 OS Synthetic.

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 PS WPI; 2004-411629/38.

XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 PS Claim 4; SEQ ID NO 116; 79pp; English.

XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.5e-07;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRRFIGSIWRFIRAFYG 18

RESULT 12

ADO34297
 ID ADO34297 standard; peptide; 18 AA.

XX

AC ADO34297;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 74; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.1e-07;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRKFLGSIWRFIRAFYG 18

RESULT 13

ADO34244

ID ADO34244 standard; peptide; 18 AA.

XX

AC ADO34244;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 21; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,

CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.1e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFYG 18
 |||||:|||||:|||||
 Db 1 GRRFLGAIWRFIRSFYG 18

RESULT 14

ADO34276
 ID ADO34276 standard; peptide; 18 AA.

XX
 AC ADO34276;

XX
 DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1..18
 FT /note= "All Lys residues are DiMethyl-Lysine"

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 53; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.1e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFYG 18
 |||||:|||||:|||||
 Db 1 GIKRFLGSIWRFIKAFYG 18

RESULT 15

ADO34227

ID ADO34227 standard; peptide; 18 AA.

XX
 AC ADO34227;

XX
 DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking related R18L linear peptide.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX
 PN 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 4; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

SQ Query Match 91.8%; Score 90; DB 8; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1e-06;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18
 |||||
 Db 1 GIRRFLGSIWRFIRAFVG 18

Search completed: March 29, 2006, 01:44:08
 Job time : 159.75 secs

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 01:44:43 ; Search time 26.4375 Seconds
(without alignments)
65.509 Million cell updates/sec

Title: US-10-712-447-5

Perfect score: 98

Sequence: 1 GIRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	49.0	627	S76462	hypothetical prote
2	45	45.9	178	A75578	transcription regu
3	44	44.9	461	G64537	2-oxoglutarate/mal
4	44	44.9	589	A34341	poly(3-hydroxybuty
5	44	44.9	806	A84060	leucyl-tRNA synthe
6	44	44.9	861	H64102	leucine-tRNA ligas
7	43.5	44.4	1025	AH3568	acriflavin resista
8	43	43.9	265	T32316	hypothetical prote
9	43	43.9	489	B84733	probable cytochrom
10	43	43.9	516	T33269	hypothetical prote
11	43	43.9	812	A46417	NIPI protein - yea
12	43	43.9	1607	T04583	TMV resistance pro
13	42.5	43.4	407	T12085	reverse transcript
14	42.5	43.4	760	E84953	penicillin-binding
15	42	42.9	107	T52113	probable transcrip
16	42	42.9	214	D72540	hypothetical prote
17	42	42.9	228	T15530	hypothetical prote
18	42	42.9	237	B73692	hypothetical prote
19	42	42.9	246	I54412	MHC HLA-A cell sur
20	42	42.9	258	F71707	o-antigen export s
21	42	42.9	258	D97700	o-antigen export s
22	42	42.9	273	HLHU69	MHC class I histoc
23	42	42.9	365	HLHUA2	MHC class I histoc
24	42	42.9	365	I38443	gene HLA-A-0203 pr
25	42	42.9	365	I61902	MHC class I histoc
26	42	42.9	365	I37542	MHC class I histoc
27	42	42.9	365	I84448	MHC class I histoc
28	42	42.9	365	I61857	MHC HLA-A2.4a chai
29	42	42.9	365	I38442	gene HLA-A-0205 pr

ALIGNMENTS

RESULT 1

S76462

hypothetical protein - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S76462

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis

S.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76462

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-627 <KAN>

A:Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:P90915; GB:AB001339; NID

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;

Best Local Similarity 38.9%; Pred. No. 8.1;

Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GIRRFLGSIWRFIRAFYG 18

Db 597 GLEQLGKIQWLQKFG 614

| : : | | | | | : | : |

RESULT 2

A75578

transcription regulator, MarR family - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: A75578

R:White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: A75578

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-178 <WHI>

A:Cross-references: UNIPROT:Q9RYR0; UNIPARC:UPI00000D3BB4; GB:AE001863; NID

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRA0248

A:Map position: 2

Query Match 45.9%; Score 45; DB 2; Length 178;

Best Local Similarity 69.2%; Pred. No. 7.2;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IRREFLSIWRFR 14
Db 23 ILRFLGGIWRLLNR 35

RESULT 3
G64537
2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)
C/Species: Helicobacter pylori
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: G64537
R/Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKernan, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A/Reference number: A64520; MUID:97394467; PMID:9252185
A/Accession: G64537
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-461 <TOM>
A/Cross-references: UNIPARC:UPI0000174217; GB:A5000511; TIGR:HP0143
C/Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IRREFLSIWRFR 14
Db 297 VRLLSWFWRPVR 309

RESULT 4
A34341
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C/Species: Alcaligenes eutrophus
C/Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C/Accession: A34341; A39190
R/Peoples, O.P.; Sinskey, A.J.
J. Biol. Chem. 264, 15298-15303, 1989
A/Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident
A/Reference number: A34341; MUID:89359357; PMID:2670936
A/Accession: A34341
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-589 <PEO>
A/Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:
A/Experimental source: strain H16
R/Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
A/Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosyn
omoter.
A/Reference number: A39190; MUID:91100279; PMID:1987116
A/Accession: A39190
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-219 <SCH>
A/Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:
A/Note: the authors translated the codon TAC for residue 120 as Thr
C/Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C/Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy 3 RRFLGSIW-----RPTRAFY 17
||| | | | | | | | | |

Best Local Similarity 69.2%; Pred. No. 7.2;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IRREFLSIWRFR 14
Db 23 ILRFLGGIWRLLNR 35

RESULT 3
G64537
2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)
C/Species: Helicobacter pylori
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: G64537
R/Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKernan, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A/Reference number: A64520; MUID:97394467; PMID:9252185
A/Accession: G64537
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-461 <TOM>
A/Cross-references: UNIPARC:UPI0000174217; GB:A5000511; TIGR:HP0143
C/Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IRREFLSIWRFR 14
Db 297 VRLLSWFWRPVR 309

RESULT 4
A34341
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C/Species: Alcaligenes eutrophus
C/Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C/Accession: A34341; A39190
R/Peoples, O.P.; Sinskey, A.J.
J. Biol. Chem. 264, 15298-15303, 1989
A/Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident
A/Reference number: A34341; MUID:89359357; PMID:2670936
A/Accession: A34341
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-589 <PEO>
A/Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:
A/Experimental source: strain H16
R/Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
A/Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosyn
omoter.
A/Reference number: A39190; MUID:91100279; PMID:1987116
A/Accession: A39190
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-219 <SCH>
A/Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:
A/Note: the authors translated the codon TAC for residue 120 as Thr
C/Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C/Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy 3 RRFLGSIW-----RPTRAFY 17
||| | | | | | | | | |

Db 100 RRFAGDAWRNTLPYRFAAFY 120

RESULT 5

A84060
leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: A84060

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: A84060

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-806 <STO>

A/Cross-references: UNIPROT:Q9K789; UNIPARC:UPI0000136555; GB:BA000004; NID:

A/Experimental source: strain C-125

C/Genetics:

A/Gene: leuS

C/Superfamily: leucine-tRNA ligase

Query Match 44.9%; Score 44; DB 2; Length 806;

Best Local Similarity 53.8%; Pred. No. 45;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRREFLSIWRFI 13
| | | | | : | | |

Db 622 GARRFLDRVWRL 634

RESULT 6

H64102
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)

N/Alternate names: leucyl-tRNA synthetase

C/Species: Haemophilus influenzae

C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C/Accession: H64102

R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, M

A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A/Reference number: A64000; MUID:95350630; PMID:7542800

A/Accession: H64102

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-861 <TIGR>

A/Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:L42023; NID:915

C/Genetics:

A/Gene: leuS

C/Superfamily: leucine-tRNA ligase

C/Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.9%; Score 44; DB 2; Length 861;

Best Local Similarity 46.2%; Pred. No. 48;

Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRREFLSIWRFI 13
| | | | | : | | |

Db 665 GAKRFLGRVWNLV 677

RESULT 7

AH3568
acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C/Accession: AH3568

R/Delvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I

; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3568
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1025 <KUR>
A:Cross-references: UNIPROT:Q8YQ05; UNIPARC:UPI00000584C8; GB:AE008918; PIDN:AAL53715.1;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME110473
A:Map position: 11
C:Superfamily: hypothetical protein b2075

Query Match 44.4%; Score 43.5; DB 2; Length 1025;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 8; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

QY 5 FLGSIWRFI---RAFY 17
Db 531 FLGSVMSFWTLPRSF 546

RESULT 8
T32316
hypothetical protein F31F4.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
A:Accession: T32316
R:Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of *C. elegans* cosmid F31F4.
A:Reference number: Z21149
A:Accession: T32316
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-265 <BLA>
A:Cross-references: UNIPROT:O17136; UNIPARC:UPI000007D19A; EMBL:AF024503; PIDN:AAB70384.
A:Experimental source: strain Bristol N2; clone F31F4
C:Genetics:
A:Gene: CESP:F31F4.4
A:Map position: 5
A:Introns: 13/3; 67/2
C:Superfamily: *Caenorhabditis elegans* hypothetical protein T09F5.1

Query Match 43.9%; Score 43; DB 2; Length 265;
Best Local Similarity 53.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFY 18
Db 253 LASLWAFVHAFEG 265

RESULT 9
B84733
probable cytochrome P450 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
A:Accession: B84733
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84733
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-489 <STO>
A:Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:G3831452; PI
C:Genetics:
A:Gene: At2g32440

A:Map position: 2
C:Superfamily: *Synechocystis* cytochrome P450 slr0574; cytochrome P450 homology

Query Match 43.9%; Score 43; DB 2; Length 489;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAF 16
Db 54 IGNNWSELRAP 64

RESULT 10

T33269
hypothetical protein C24B9.13 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
A:Accession: T33269
R:Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of *C. elegans* cosmid C24B9.
A:Reference number: Z21310
A:Accession: T33269
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-516 <MUR>
A:Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.
A:Experimental source: strain Bristol N2; clone C24B9
C:Genetics:
A:Gene: CESP:C24B9.13
A:Map position: 5
A:Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2

Query Match 43.9%; Score 43; DB 2; Length 516;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRRELGSIWRFIRAFY 18
Db 252 LKFFITSILWMPHAFDG 268

RESULT 11

A46417
NIP1 protein - yeast (*Saccharomyces cerevisiae*)
A:Alternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; prote
C:Species: *Saccharomyces cerevisiae*
C:Date: 21-Sep-1993 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
A:Accession: A46417; S53979; S59302
R:Gu, Z.; Moerschell, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A:Title: NIP1, a gene required for nuclear transport in yeast.
A:Reference number: A46417; MUID:93066237; PMID:1332047
A:Accession: A46417
A:Molecule type: DNA
A:Residues: 1-812 <GUL>
A:Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:L02899
A:Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBI:P:117850)

R:Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, April 1995
A:Reference number: S53969
A:Accession: S53979
A:Molecule type: DNA
A:Residues: 571-582, 'Q', 584-640, 'K', 642, 'K', 644-812 <CON>
A:Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:G798940; PID:G798951; MIPS:Y
R:Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A:Reference number: S59302
A:Accession: S59302
A:Molecule type: DNA
A:Residues: 1-110, 'V', 112-582, 'Q', 584-602 <CHU>
A:Cross-references: UNIPARC:UPI0000168ACA; EMBL:Z54141; NID:G1072408; PID:G984682; MIPS
A:Experimental source: strain AB972

GN Name=rzcb;
 OS Rhizobium leguminosarum (biovar viciae).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OK NCBI_TaxID=387;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=305;
 RX MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
 RA Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
 RT "Analysis of the genetic region encoding a novel rhizobiotin from
 RT Rhizobium leguminosarum bv. viciae strain 305.";
 RL Can. J. Microbiol. 47:495-502(2001).
 DR EMBL; AF273216; AAC25076.1; -; Genomic_DNA.
 DR HSSP; P08716; 1MT0.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005524; F: ATP binding; IEA.
 DR GO; GO:0016887; F: ATPase activity; IEA.
 DR GO; GO:0042626; F: ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F: nucleotide binding; IEA.
 DR GO; GO:0008233; F: peptidase activity; IEA.
 DR GO; GO:0008565; F: protein transporter activity; IEA.
 DR GO; GO:0015031; P: protein transport; IEA.
 DR GO; GO:0006508; P: proteolysis and peptidolysis; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR011527; ABC_membrane_1.
 DR InterPro; IPR001140; ABC_TM_transp.
 DR InterPro; IPR003439; ABC_transp_like.
 DR InterPro; IPR005074; Peptidase_C39.
 DR InterPro; IPR010132; Type I_sec_HlyB.
 DR Pfam; PF00664; ABC_membrane_1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR Pfam; PF03412; Peptidase_C39; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRfam; TIGR01846; type I sec HlyB; 1.
 DR PROSITE; PS09029; ABC_TMIF_1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 DR PROSITE; PS05090; PEPTIDASE_C39; 1.
 DR PS05090; PEPTIDASE_C39; 1.
 SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;
 Query Match 53.1%; Score 52; DB 2; Length 735;
 Best Local Similarity 62.5%; Pred. No. 17;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GIRRFGLSIWRFIRAF 16
 Db 161 GFRWFLPAIWRYRAF 176
 |||:|||||
 |||:|||||
 RESULT 3
 Q4LK44_9BURK PRELIMINARY; PRT; 408 AA.
 AC Q4LK44;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=Bcen2424DRAFT.1071;
 OS Burkholderia cenocepacia H12424.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
 OK NCBI_TaxID=331272;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=H12424;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
 RT H12424.";
 RT Submitted (JUN-2005) to the ENBL/GenBank/DBJ databases.
 RL

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=H12424;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
 RT H12424.";
 RL Submitted (JUN-2005) to the ENBL/GenBank/DBJ databases.
 CC -I- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAHL0100063; EAM16412.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;
 Query Match 52.0%; Score 51; DB 2; Length 408;
 Best Local Similarity 47.1%; Pred. No. 13;
 Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GIRRFGLSIWRFIRAF 17
 Db 328 GIRQMLGHVWQWTRSS 344
 |||:|||||
 |||:|||||
 RESULT 4
 Q5GH72_HUMAN PRELIMINARY; PRT; 579 AA.
 ID Q5GH72_HUMAN PRELIMINARY;
 AC Q5GH72;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE XK-related protein 7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Huang C.-H., Chen Y.;
 RT "A superfamily of XK-related genes (XRG) widely expressed in
 RT vertebrates and invertebrates.";
 RL Submitted (JAN-2004) to the ENBL/GenBank/DBJ databases.
 DR EMBL; AY534245; AAT07094.1; -; mRNA.
 SQ SEQUENCE 579 AA; 63825 MW; D8D0FF64B9EDD53D CRC64;
 Query Match 51.0%; Score 50; DB 2; Length 579;
 Best Local Similarity 58.3%; Pred. No. 28;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 6 LGSIWRFIRAF 17
 Db 190 LGQVWRYRALY 201
 |||:|||||
 |||:|||||
 RESULT 5
 Q5GH56_RAT PRELIMINARY; PRT; 580 AA.
 ID Q5GH56_RAT PRELIMINARY;
 AC Q5GH56;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE XK-related protein 7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley;
 RA Huang C.-H., Chen Y.;
 RT "A superfamily of XK-related genes (XRG) widely expressed in

```
RT vertebrates and invertebrates." ;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY534261; AAT07110.1; -; mRNA.
SQ SEQUENCE 580 AA; 64337 MW; 8F4907F391B4F5BE CRC64;

Query Match 51.0%; Score 50; DB 2; Length 580;
Best Local Similarity 58.3%; Pred. No. 28;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAFY 17
Db 190 LGQVWRYLRALY 201

RESULT 6
Q5GH64 MOUSE PRELIMINARY; PRT; 580 AA.
AC Q5GH64;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE XK-related protein 7.
GN Name=AY534253;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
vertebrates and invertebrates." ;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY534253; AAT07102.1; -; mRNA.
DR MGI; MGI:3526711; AY534253.
SQ SEQUENCE 580 AA; 64301 MW; F3291FABF4C5A826 CRC64;

Query Match 51.0%; Score 50; DB 2; Length 580;
Best Local Similarity 58.3%; Pred. No. 28;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAFY 17
Db 190 LGQVWRYLRALY 201

RESULT 7
Q84ZW1 PEA PRELIMINARY; PRT; 488 AA.
AC Q84ZW1;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Ent-kaurenoic acid oxidase.
GN Name=KA01;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
OX NCBI_TaxID=3889;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Shoot;
RX MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;
RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;
RT "The pea gene NA encodes ent-kaurenoic acid oxidase." ;
RL Plant Physiol. 131:335-344 (2003).
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By
similarity).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AF537321; AAO23063.1; -; mRNA.
```

```
DR GO; GO:0046872; P:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Endoplasmic reticulum; Heme; Iron; Metal-binding; Monooxygenase;
KW Oxidoreductase.
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 488;
Best Local Similarity 58.3%; Pred. No. 34;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FLGSIWRFIRAF 16
Db 54 FIGNWSFLRAF 65

RESULT 8
Q4NQH4_9DELT PRELIMINARY; PRT; 188 AA.
AC Q4NQH4;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Sigma-70 region 2.
GN ORFNames=AdelHRAFT_0950;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cytophacteria; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Istrati S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C." ;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
dehalogenans 2CP-C." ;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAHD0100035; EAL77797.1; -; Genomic DNA.
SQ SEQUENCE 188 AA; 21278 MW; 6DEAFDBF874C4721 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 188;
Best Local Similarity 30.6%; Pred. No. 18;
Matches 11; Conservative 4; Mismatches 3; Indels 18; Gaps 1;

Qy 1 GIRPFLGSI-----WRFIRAFY 18
Db 30 GVRRLGSLVLRDGDADAYARFESLWRLPAFRG 65

RESULT 9
Q8R587 MOUSE PRELIMINARY; PRT; 298 AA.
ID Q8R587 MOUSE
AC Q8R587;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
```

```

RT   vertebrates and invertebrates.",
RL   Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AY534268; AAT07117.1; -, mRNA.
SQ   SEQUENCE 578 AA; 66214 MW; 8915B2A30D38E80D CRC64;

Query Match          49.0%; Score 48; DB 2; Length 578;
Best Local Similarity 58.3%; Pred. No. 58;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY   6 LGSIMRFIRAFY 17
DB   185 LGQVRYIRTM 196
      ||-|||:|
      ||-|||:|

RESULT 11
P74489 SYN93
ID   P74489 SYN93 PRELIMINARY; PRT; 627 AA.
AC   P74489
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   S111858 protein.
GN   OrderedLocusNames=sl11858;
OS   Synchocystis sp. (strain PCC 5803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
ON   NCBI_TaxID=1148;
RX   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE-97061201; PubMed=8905231;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hiroseawa M., Sugiyama M., Saeamato S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA   Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA   Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synchocystis sp. strain PCC5803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
DR   EMBL; BA000022; BAA18591.1; -, Genomic_DNA.
DR   PIR; S76462; S76462.
KW   Complete proteome.
SQ   SEQUENCE 627 AA; 69724 MW; BBE187A53BF96229 CRC64;

Query Match          49.0%; Score 48; DB 2; Length 627;
Best Local Similarity 38.9%; Pred. No. 64;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY   1 GTRFLGSIWIRAFY 18
DB   597 GLEQLLGKIWMLRQKFG 614
      |:|:|:|:|:|
      |:|:|:|:|:|

RESULT 12
P97035 HAESO
ID   P97035 HAESO PRELIMINARY; PRT; 240 AA.
AC   P97035
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Orf13; not preceded by a good RBS site (Fragment).
DE   Haemophilus somnus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC   Pasteurellaceae; Histophilus.
ON   NCBI_TaxID=731;
RX   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   STRAIN=HS25;
RX   MEDLINE=97221585; PubMed=9068631;
RA   Pontarollo R.A., Rioux C.R., Potter A.A.;
RT   "Cloning and characterization of bacteriophage-like DNA from
RT   Haemophilus somnus homologous to phages P2 and HPI.";
RA   J. Bacteriol. 179:1872-1879(1997).
RX   [2]

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HS25;
RA Pontarollo R.A.;
RL Thesis (1996); V. I. D. O., University of Saskatchewan.
DR EMBL; U28154; AAC45167.1; -; Genomic_DNA.
FT NON TER 240 240
SQ SEQUENCE 240 AA; 26610 MW; 63348D8619BBAC30 CRC64;

Query Match 48.5%; Score 47.5; DB 2; Length 240;
Best Local Similarity 57.9%; Pred. No. 28;
Matches 11; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 1 GIRRFGLSINRIFIR-AFYG 18
|||:|||||:|:|:
Db 201 GTFQFLGGIWEHKEAFNG 219
|||:|||||:|:|:

RESULT 13
Q5U414_XENLA
ID Q5U414_XENLA PRELIMINARY; PRT; 486 AA.
AC Q5U414_
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE LOC495492 protein (fragment).
GN Name=LOC495492;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xeropodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchwood J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gricham J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smal M.A.;
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX Klein S., Gerhard D.S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; BC085081; AAH85081.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005355; F:glucose transporter activity; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0008643; P:carbohydrate transport; IEA.
DR InterPro; IPR000803; Gluc_transporter.
DR InterPro; IPR007114; MFS_transporter.
DR InterPro; IPR005826; Sub_transporter.
DR InterPro; IPR003663; Sug_transpt.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; Sugar tr; 1.
DR PRINTS; PR00172; GLUCRNSPORT.
DR PRINTS; PR00171; SUGRNSPORT.
DR TIGRfams; TIGR00879; SP; 1.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
DR KW Sugar transport; Transmembrane; Transport.
FT NON TER 1
SQ SEQUENCE 486 AA; 54035 MW; E333F97CD90A1119 CRC64;

Query Match 48.0%; Score 47; DB 2; Length 486;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 1 GIRRFGLS--IWRIFRAF 16
|:|:|||||:|:|:
Db 174 GLREFLGSETLWPLYMAP 191
|:|:|||||:|:|:

RESULT 14
Q5ZDS6_ORYSA
ID Q5ZDS6_ORYSA PRELIMINARY; PRT; 910 AA.
AC Q5ZDS6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Fucate leucyl-cRNA synthetase.
GN Name=P0698A04.32;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niumura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Ito S., Ito T., Ito Y., Iwabuchi A., Kamiya K.,
RA Karasawa K., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takasaki Y., Terasawa K., Teuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA (Leu) = AMP +
CC diphosphate + L-leucyl-tRNA(Leu).
DR EMBL; AP002858; BAD52586.1; -; Genomic_DNA.
DR Gramene; Q5ZDS6; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu-tRNAsynt1a.
DR InterPro; IPR002300; tRNA-synt_1a.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00985; TRNASYNTHLEU.

DR TIGRFAMs; TIGR00396; leuS_bact; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Nucleotide-binding;
KW Protein biosynthesis.
SQ SEQUENCE 910 AA; 102551 MW; E5856521EC817196 CRC64;

Query Match 48.0%; Score 47; DB 2; Length 910;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRPI 13
: : : : :
Db 722 GVHFLGRTWRLV 734

RESULT 15
Q5ZPA2 9DELT PRELIMINARY; PRT; 385 AA.
AC Q5ZPA2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Angiococcus disciformis.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Cystobacteraceae; Cystobacter.
OX NCBI_TaxID=38;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=An d48;
RX PubMed=15324808; DOI=10.1016/j.chembiol.2004.05.014;
RA Sandmann A.; Sasse F.; Mueller R.;
RT "Identification and analysis of the core biosynthetic machinery of
RT tubulysein, a potent cytotoxin with potential anticancer activity.";
RL Chem. Biol. 11:1071-1079(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=An d48;
RA Sandmann A.;
RT "Identifizierung und Charakterisierung des Tubulysein
RT Biosynthesegencusters aus dem Myxobakterium Angiococcus disciformis
RT An d48.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ620477; CAF05655.1; -; Genomic_DNA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR SMART; SM00247; XTALbg; 1.
DR PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 385 AA; 43283 MW; CB609F2D64027CA0 CRC64;

Query Match 46.9%; Score 46; DB 2; Length 385;
Best Local Similarity 42.9%; Pred. No. 80;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 5 FLGSIWRPIAFY 18
: : : : :
Db 66 YLGDVWRYTKRTYG 79

Search completed: March 29, 2006, 01:49:11
Job time : 168.938 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 01:49:32 ; Search time 37.6875 Seconds
(without alignments)
39.487 Million cell updates/sec

Title: US-10-712-447-5

Perfect score: 98

Sequence: 1 GIRFLGSIWIRAFYFG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	79.6	18	2	US-08-940-095-242 Sequence 242, App
2	78	79.6	18	2	US-08-940-093-242 Sequence 242, App
3	78	79.6	18	2	US-08-940-096-242 Sequence 242, App
4	78	79.6	18	2	US-09-465-719-242 Sequence 242, App
5	78	79.6	18	2	US-09-453-608-242 Sequence 242, App
6	78	79.6	18	2	US-09-453-838-242 Sequence 242, App
7	78	79.6	18	2	US-08-940-136-242 Sequence 242, App
8	78	79.6	18	2	US-09-453-841-242 Sequence 242, App
9	78	79.6	18	2	US-09-453-833-242 Sequence 242, App
10	78	79.6	18	2	US-09-453-826-242 Sequence 242, App
11	78	79.6	18	2	US-09-453-840-242 Sequence 242, App
12	78	79.6	18	2	US-09-865-989-242 Sequence 242, App
13	78	79.6	18	2	US-09-453-834-242 Sequence 242, App
14	78	79.6	18	2	US-10-283-599-242 Sequence 242, App
15	78	79.6	18	2	US-09-465-718-242 Sequence 242, App
16	51	52.0	76	2	US-09-205-258-892 Sequence 892, App
17	51	52.0	76	2	US-10-004-860-892 Sequence 892, App
18	47.5	48.5	253	2	US-09-586-106D-49 Sequence 49, Appl
19	47.5	48.5	253	2	US-10-799-870-49 Sequence 49, Appl
20	45.5	46.4	254	2	US-09-586-106D-45 Sequence 45, Appl
21	45.5	46.4	254	2	US-10-799-870-45 Sequence 45, Appl
22	45	45.9	22	1	US-08-338-882-40 Sequence 40, Appl
23	45	45.9	22	1	US-08-338-882-41 Sequence 41, Appl
24	45	45.9	539	2	US-09-710-279-340 Sequence 340, App
25	45	45.9	835	2	US-09-134-001C-5105 Sequence 5105, Ap
26	45	45.9	877	2	US-09-328-352-8162 Sequence 8162, Ap
27	44	44.9	22	1	US-08-132-767-50 Sequence 50, Appl

28	44	44.9	589	1	US-08-756-317-5	Sequence 5, Appli
29	44	44.9	1052	2	US-09-134-000C-6620	Sequence 6620, Ap
30	43	43.9	23	2	US-10-360-101-83	Sequence 83, Appl
31	43	43.9	683	2	US-09-902-1540-15932	Sequence 15932, A
32	43	43.9	812	2	US-09-538-092-643	Sequence 643, App
33	42	42.9	14	1	US-08-480-190-3	Sequence 3, Appli
34	42	42.9	14	1	US-08-488-379-3	Sequence 3, Appli
35	42	42.9	14	2	US-08-475-399A-3	Sequence 3, Appli
36	42	42.9	14	2	US-08-077-255A-3	Sequence 3, Appli
37	42	42.9	14	4	PCT-US93-07545-3	Sequence 2, Appli
38	42	42.9	15	1	US-08-480-190-2	Sequence 2, Appli
39	42	42.9	15	1	US-08-488-379-2	Sequence 2, Appli
40	42	42.9	15	2	US-08-475-399A-2	Sequence 2, Appli
41	42	42.9	15	2	US-08-077-255A-2	Sequence 2, Appli
42	42	42.9	15	4	PCT-US93-07545-2	Sequence 2, Appli
43	42	42.9	18	1	US-08-480-190-1	Sequence 1, Appli
44	42	42.9	18	1	US-08-480-190-61	Sequence 61, Appli
45	42	42.9	18	1	US-08-488-379-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-940-095-242
; Sequence 242, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DISLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/POCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
US-08-940-095-242

```
Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   ||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 2
US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   ||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 3
US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
```

```
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; US-08-940-096-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   ||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465.719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265377e
US-09-465-719-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,605
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-605-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
; US-09-453-838-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIKAFVG 18
|::|::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 7

US-08-940-136-242
; Sequence 242, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
US-08-940-136-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIKAFVG 18
|::|::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 8

US-09-453-841-242
; Sequence 242, Application US/09453841

; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e
US-09-453-841-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIKAFVG 18
|::|::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 9

US-09-453-833-242
; Sequence 242, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas

Wed Mar 29 18:01:20 2006

```

; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-5556
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6602854e
; US-09-453-833-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGLSGIWRFIKAFVG 18
   ||::|||::|||::|||
Db 1 GIKRFLGSIWKFIKAFVG 18

RESULT 11
US-09-453-840-242
; Sequence 242, Application US/09453840
; Patent No. 6716816
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-5556
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6602854e
; US-09-453-833-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGLSGIWRFIKAFVG 18
   ||::|||::|||::|||
Db 1 GIKRFLGSIWKFIKAFVG 18

RESULT 10
US-09-453-826-242
; Sequence 242, Application US/09453826
; Patent No. 6630450
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,826
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRPIAFVG 18
|::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:

US-09-865-989-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRPIAFVG 18
|::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
; US-09-453-834-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRPIAFVG 18
|::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; USE TO TREAT DYSLIPIDEMIC DISORDERS.
```

```
;
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283.599
; FILING DATE: 29-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940.136
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-5556
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6844327e
; US-10-283-599-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
   |::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15
US-09-465-718-242
; Sequence 242, Application US/09465718
; Patent No. 6900177
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,718
```

```
;
; FILING DATE: 17-Dec-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6900177e
; US-09-465-718-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
   |::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: March 29, 2006, 01:51:15
Job time : 38.6875 secs
```

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 02:05:02 ; Search time 153 Seconds
(without alignments)
49.156 Million cell updates/sec

Title: US-10-712-447-5

Perfect score: 98

Sequence: 1 GIRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-2
2	98	100.0	18	4	US-10-712-447-5
3	98	100.0	18	4	US-10-712-447-8
4	98	100.0	18	4	US-10-712-447-10
5	98	100.0	18	4	US-10-712-447-13
6	95	96.9	18	4	US-10-712-447-91
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-117
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	92	93.9	18	4	US-10-712-447-21
13	92	93.9	18	4	US-10-712-447-53
14	92	93.9	18	4	US-10-712-447-74
15	90	91.8	18	4	US-10-712-447-4
16	90	91.8	18	4	US-10-712-447-127
17	89	90.8	18	4	US-10-712-447-99
18	88	89.8	18	4	US-10-712-447-18
19	88	89.8	18	4	US-10-712-447-112
20	88	89.8	18	4	US-10-712-447-113
21	88	89.8	18	4	US-10-712-447-114
22	87	88.8	18	4	US-10-712-447-17
23	86	87.8	18	4	US-10-712-447-61
24	86	87.8	18	4	US-10-712-447-82
25	85	86.7	18	4	US-10-712-447-16
26	85	86.7	18	4	US-10-712-447-96
27	85	86.7	18	4	US-10-712-447-121

28	84	85.7	18	4	US-10-712-447-22	Sequence 22, Appl
29	84	85.7	18	4	US-10-712-447-78	Sequence 78, Appl
30	84	85.7	18	4	US-10-712-447-95	Sequence 95, Appl
31	84	85.7	18	4	US-10-712-447-120	Sequence 120, Appl
32	82	83.7	18	4	US-10-712-447-19	Sequence 19, Appl
33	82	83.7	18	4	US-10-712-447-56	Sequence 56, Appl
34	82	83.7	18	4	US-10-712-447-58	Sequence 58, Appl
35	82	83.7	18	4	US-10-712-447-77	Sequence 77, Appl
36	82	83.7	18	4	US-10-712-447-79	Sequence 79, Appl
37	82	83.7	18	4	US-10-712-447-80	Sequence 80, Appl
38	82	83.7	18	4	US-10-712-447-94	Sequence 94, Appl
39	81	82.7	18	4	US-10-712-447-57	Sequence 57, Appl
40	81	82.7	18	4	US-10-712-447-100	Sequence 100, Appl
41	80	81.6	18	4	US-10-712-447-41	Sequence 41, Appl
42	79	80.6	18	4	US-10-712-447-97	Sequence 97, Appl
43	78	79.6	18	3	US-09-865-989-242	Sequence 242, App
44	78	79.6	18	3	US-09-865-989-242	Sequence 242, App
45	78	79.6	18	4	US-10-099-574A-242	Sequence 242, App

ALIGNMENTS

RESULT 1

US-10-712-447-2
; Sequence 2, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURES:
; OTHER INFORMATION: c-term amidated
US-10-712-447-2

Query Match 100.0%; Score 98; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 8.8e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0;

QY 1 GIRRFLGSIWRFIRAFYG 18

DB 1 GIRRFLGSIWRFIRAFYG 18

RESULT 2

US-10-712-447-5
; Sequence 5, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 3
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 4
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210

; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 5
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 6
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18

```

RESULT 10
US-10-712-447-129
; Sequence 129, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GABBER, DAVID W.
; APPLICANT: DATTI, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 129
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-129

```

```
Query Match      95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.5e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||
Db 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||

RESULT 11
US-10-712-447-131
; Sequence 131, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-712-447-131

Query Match      95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.5e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||
Db 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||

RESULT 12
US-10-712-447-21
; Sequence 21, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-712-447-21

Query Match      93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.1e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||
Db 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||

RESULT 13
US-10-712-447-53
; Sequence 53, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 53
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-712-447-53

Query Match      93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.1e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||
Db 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||

RESULT 14
US-10-712-447-74
; Sequence 74, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-712-447-74
```

Wed Mar 29 18:01:20 2006

```
; OTHER INFORMATION: peptide
US-10-712-447-74
Query Match      93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.1e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
   |||:|||:|||:|||
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 15
US-10-712-447-4
; Sequence 4, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-4
Query Match      91.8%; Score 90; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
   |||:|||:|||:|||
Db 1 GIRRFLGSIWRFIRAFVG 18

Search completed: March 29, 2006, 02:10:39
Job time : 153 secs
```

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 02:06:17 ; Search time 16.875 Seconds
(without alignments)
31.461 Million cell updates/sec

Title: US-10-712-447-5

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pap.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pap.*
- 4: /SIDSS/ptodata/1/pubpaa/PCT_NEW PUB.pap.*
- 5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pap.*
- 6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pap.*
- 7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pap.*
- 8: /SIDSS/ptodata/1/pubpaa/US60_NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	45.9	306	7	US-11-096-568A-16673
2	45	45.9	327	7	US-11-096-568A-16672
3	45	45.9	360	7	US-11-096-568A-16671
4	45	45.9	539	6	US-10-793-626-340
5	44	44.9	379	5	US-09-978-360A-506
6	42	42.9	85	7	US-11-172-740-229
7	42	42.9	365	6	US-10-821-234-1575
8	42	42.9	805	6	US-10-485-517-198
9	41	41.8	265	6	US-10-392-234A-54
10	41	41.8	394	7	US-11-087-099-521
11	41	41.8	394	7	US-11-087-099-1491
12	41	41.8	394	7	US-11-087-099-1644
13	41	41.8	394	7	US-11-087-099-1700
14	41	41.8	394	7	US-11-087-099-2589
15	41	41.8	394	7	US-11-087-099-2733
16	41	41.8	394	7	US-11-087-099-3648
17	41	41.8	394	7	US-11-087-099-4073
18	41	41.8	394	7	US-11-087-099-4652
19	41	41.8	394	7	US-11-087-099-4677
20	41	41.8	394	7	US-11-087-099-4777
21	41	41.8	394	7	US-11-087-099-4910
22	41	41.8	394	7	US-11-087-099-6008
23	41	41.8	394	7	US-11-087-099-6227
24	41	41.8	394	7	US-11-087-099-6781
25	41	41.8	394	7	US-11-087-099-6911

```

26 41 41.8 394 7 US-11-087-099-7139 Sequence 7139, Ap
27 41 41.8 394 7 US-11-087-099-7287 Sequence 7287, Ap
28 41 41.8 394 7 US-11-087-099-7806 Sequence 7806, Ap
29 41 41.8 394 7 US-11-087-099-7928 Sequence 7928, Ap
30 41 41.8 394 7 US-11-087-099-8706 Sequence 8706, Ap
31 41 41.8 394 7 US-11-087-099-8837 Sequence 8837, Ap
32 41 41.8 394 7 US-11-087-099-9004 Sequence 9004, Ap
33 41 41.8 394 7 US-11-087-099-9271 Sequence 9271, Ap
34 41 41.8 394 7 US-11-087-099-9973 Sequence 9973, Ap
35 41 41.8 394 7 US-11-087-099-10104 Sequence 10104, A
36 41 41.8 394 7 US-11-087-099-10325 Sequence 10325, A
37 41 41.8 394 7 US-11-087-099-10517 Sequence 10517, A
38 41 41.8 394 7 US-11-087-099-11001 Sequence 11001, A
39 41 41.8 394 7 US-11-087-099-11036 Sequence 11036, A
40 41 41.8 394 7 US-11-087-099-11514 Sequence 11514, A
41 41 41.8 394 7 US-11-087-099-11905 Sequence 11905, A
42 41 41.8 394 7 US-11-087-099-12199 Sequence 12199, A
43 41 41.8 394 7 US-11-087-099-12453 Sequence 12453, A
44 41 41.8 499 7 US-11-087-099-6018 Sequence 6018, Ap
45 41 41.8 514 7 US-11-096-568A-26625 Sequence 26625, A

```

ALIGNMENTS

RESULT 1

```

US-11-096-568A-16673
; Sequence 16673, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 16673
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12353656
US-11-096-568A-16673

```

```

Query Match 45.9%; Score 45; DB 7; Length 306;
Best Local Similarity 58.3%; Pred. No. 5.6;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 IRRFLGSIWRFI 13
      :| |||:|
DB      200 VRESLGSLWRPM 211

```

RESULT 2

```

US-11-096-568A-16672
; Sequence 16672, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 16672
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:

```

; NAME/KEY: misc feature
; LOCATION: (1)..(327)
; OTHER INFORMATION: Ceres Seq. ID no. 12353655
US-11-096-568A-16672

Query Match 45.9%; Score 45; DB 7; Length 327;
Best Local Similarity 58.3%; Pred. No. 6;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFI 13
; :| :||| :|||
Db 221 VRESLGLSWRFM 232

RESULT 3
US-11-096-568A-16671
; Sequence 16671, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 16671
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(360)
; OTHER INFORMATION: Ceres Seq. ID no. 12353654
US-11-096-568A-16671

Query Match 45.9%; Score 45; DB 7; Length 360;
Best Local Similarity 58.3%; Pred. No. 6.5;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFI 13
; :| :||| :|||
Db 254 VRESLGLSWRFM 265

RESULT 4
US-10-793-626-340
; Sequence 340, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 340
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-340

Query Match 45.9%; Score 45; DB 6; Length 539;
Best Local Similarity 61.5%; Pred. No. 9.6;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFI 13

Db 357 GSRFLDRVWRLI 369
; :| :||| :|||

RESULT 5
US-09-378-360A-506
; Sequence 506, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 506
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -37..-1
US-09-378-360A-506

Query Match 44.9%; Score 44; DB 5; Length 379;
Best Local Similarity 53.3%; Pred. No. 9.9;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 RFLGSIWRFIRAFY 18
; :| :||| :|||
Db 76 RYRGSIWRFIVRACLG 90

RESULT 6
US-11-172-740-229
; Sequence 229, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
; APPLICANT: MASCIA, Peter
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; FILE REFERENCE: 2750-1602PUS2
; CURRENT APPLICATION NUMBER: US/11/172,740
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,621


```
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,800
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 229
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(81)
; OTHER INFORMATION: Pfam Name: PC4; Pfam Description: Transcriptional Coactivator p15
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for delaying flowering time
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making lethal plants for genetic confinement
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flower
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants with increased biomass and fold
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making smaller plants
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making taller plants and plants with longer
; OTHER INFORMATION: inflorescences
US-11-172-740-229

Query Match 42.9%; Score 42; DB 7; Length 85;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IRRFLGSIWRFIRAFY 17
Db 54 VRNNGKIWDIREFY 69

RESULT 7
US-10-821-234-1575
; Sequence 1575, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1575
; LENGTH: 365
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1575

Query Match 42.9%; Score 42; DB 6; Length 365;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAFY 17
Db 127 VGSDWRFRLRGVH 138

RESULT 8
US-10-485-517-198
; Sequence 198, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629W0
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 198
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-198

Query Match 42.9%; Score 42; DB 6; Length 805;
Best Local Similarity 53.8%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFI 13
Db 623 GSRRLDRVWRLM 635

RESULT 9
US-10-392-234A-54
; Sequence 54, Application US/10392234A
; Publication No. US2005025538A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia and Upjohn Corporation
; APPLICANT: Buxser, Steven
; APPLICANT: Poole, Keith
; APPLICANT: Decker, Douglas
; APPLICANT: Xiazunhi Li
; TITLE OF INVENTION: Method for Screening for acraB Transporter Family Inhibitors
; FILE REFERENCE: 6206
; CURRENT APPLICATION NUMBER: US/10/392,234A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/364,935
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-392-234A-54

Query Match 41.8%; Score 41; DB 6; Length 265;
Best Local Similarity 50.0%; Pred. No. 22;
```

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 9 IWREIRAFYG 18
||||: :|
Db 223 IWREMKVYFG 232

RESULT 10

US-11-087-099-521
; Sequence 521, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 521
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-521

Query Match 41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
:|:|:|
Db 19 VGGWMAFLRAF 29

RESULT 11

US-11-087-099-1491
; Sequence 1491, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1491
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(394)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-1491

Query Match 41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
:|:|:|
Db 19 VGGWMAFLRAF 29

RESULT 12

US-11-087-099-1644
; Sequence 1644, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22

; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1644
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-1644

Query Match 41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
:|:|:|
Db 19 VGGWMAFLRAF 29

RESULT 13

US-11-087-099-1700
; Sequence 1700, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1700
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-1700

Query Match 41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
:|:|:|
Db 19 VGGWMAFLRAF 29

RESULT 14

US-11-087-099-2589
; Sequence 2589, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2589
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-2589

Query Match 41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
:|:|:|
Db 19 VGGWMAFLRAF 29

RESULT 15

US-11-087-099-2733
; Sequence 2733, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

Wed Mar 29 18:01:21 2006

```
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2733
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-2733

Query Match      41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. NO. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      6 LGSIWRFIRAF 16
Db      19 VGGMWAFLRAF 29
      :|:|:|:|:|:|
      :|:|:|:|:|:|

Search completed: March 29, 2006, 02:11:16
Job time : 17.875 secs
```

This Page Blank (uspto)